

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model  
Run on: March 7, 2002, 16:48:39 ; Search time 4873.04 Seconds  
(without alignments)  
1604.679 Million cell updates/sec

Title: US-09-236-995D-3  
Perfect score: 474  
Sequence: 1 aacaagatgctattatggca.....gtttccatcacaaagaggttag 474

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues  
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_scs.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_om.\*
- 20: em\_or.\*
- 21: em\_ov.\*
- 22: em\_pat.\*
- 23: em\_ph.\*
- 24: em\_pl.\*
- 25: em\_ro.\*
- 26: em\_scs.\*
- 27: em\_sy.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htgo\_hum.\*
- 31: em\_htgo\_inv.\*
- 32: em\_htgo\_rod.\*
- 33: em\_htg\_hum.\*
- 34: em\_htg\_inv.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_other.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB	ID	Description
1	474	100.0	3211	8	ZMPARP2	AJ222589 Zea mays
2	474	100.0	3285	8	AF093627	AF093627 Zea mays
3	280	59.1	3187	8	ATH131705	AJ131705 Arabidops
4	158.6	33.5	1939	10	RNPARP2	X65497 R.norvegicu
5	157.6	33.2	3718	5	XELPADPRP	D14667 Frog mRNA f
6	155	33.1	3128	10	RNU94340	U94340 Rattus norv
7	157	32.7	3617	5	XLNAPRG	212139 X.laeviss PA
8	154.4	32.6	2147	8	ATPARP	248243 A.thaliana
9	153.8	32.4	3036	5	GGPADPRP	X52690 Chicken mRN
10	152.2	32.1	3845	10	BC012041	BC012041 Mus muscu
11	151.4	31.9	2295	8	ZMPARP1	AJ222588 Zea mays
12	150.6	31.8	3172	10	MMADPRP	X14206 Mouse mRNA
13	150.6	31.8	3589	4	BOVPAS	D90073 Bovine poly
14	149	31.4	1732	10	AF126717	AF126717 Mus muscu
15	147.4	31.1	3047	10	AF168781	AF168781 Crictetu
16	142.6	30.1	1771	9	HUMADPPO	M17081 Human place
17	142.6	30.1	3640	9	HUMFOLP	M18112 Human poly(
18	142.6	30.1	3792	6	A52134	A52134 Sequence 1
19	142.6	30.1	3795	9	HUMRISDAD	J03473 Human poly(
20	142.6	30.1	5787	9	GORADPRB	I24094 Gorilla gor
21	139.4	29.4	3045	6	AX058340	AX058340 Sequence
22	139.4	29.4	3045	6	AX062277	AX062277 Sequence
23	139.4	29.4	3660	9	HUMPPOL	M32721 Human poly(
24	139.4	29.4	3747	6	I14359	I14359 Sequence 5
25	137.8	29.1	1822	3	DMPARP5	AF051548 Drosophil
26	137.8	29.1	2682	9	S54638	S54638 (pseudogene
27	137.8	29.1	3080	3	DROADPRPA	D13806 Fruit fly m
28	137.8	29.1	5345	6	I14360	I14360 Sequence 7
29	137.8	29.1	9254	9	HUMADPRP2	L14752 Homo sapien
30	137.8	29.1	10988	2	AC014613	AC014613 Drosophil
31	137.8	29.1	16864	3	AE002892	AE002892 Drosophil
32	137.8	29.1	155026	9	AL442128	AL442128 Human DNA
33	137.4	29.0	3463	3	SPEPADPRP	D16482 Sarcophaga
34	136.2	28.7	2682	6	I14357	I14357 Sequence 3
35	122.6	25.9	687	6	AX058382	AX058382 Sequence
36	122.6	25.9	738	6	AX058380	AX058380 Sequence
37	122.6	25.9	864	6	AX058336	AX058336 Sequence
38	122.6	25.9	1754	9	HSA236912	AJ236912 Homo sapi
39	122.6	25.9	1797	9	HSA236876	AJ236876 Homo sapi
40	122.6	25.9	1814	6	AX058317	AX058317 Sequence
41	122.6	25.9	1843	6	AX008892	AX008892 Sequence
42	122.6	25.9	1874	6	AX058374	AX058374 Sequence
43	122.6	25.9	3200	6	AX058362	AX058362 Sequence
44	121	25.5	1910	9	AF085734	AF085734 Homo sapi
45	120.2	25.4	1707	6	AX058338	AX058338 Sequence

ALIGNMENTS

RESULT	1	ZMPARP2	ZMPARP2	3211 bp	mRNA	PLN	19-NOV-1997
LOCUS		Zea mays					
DEFINITION		Zea mays mRNA for poly(ADP-ribose) polymerase (3211bp).					
ACCESSION		AJ222589					
VERSION		AJ222589.1		GI:2632128			
KEYWORDS		PARP gene; poly(ADP-ribose) polymerase;					
SOURCE		Zea mays.					
ORGANISM							
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.					
REFERENCE		1 (bases 1 to 3211)					
AUTHORS		Babychuk E., Cottrill P., Storozhenko S., Fuangthong M., O'Farrell M., Van Montagu M., Inze D. and Kushnir S.					
TITLE		Higher plants possess two poly(ADP-ribose) polymerases					
JOURNAL		Unpublished					
REFERENCE		2 (bases 1 to 3211)					
AUTHORS		Kushnir S.					
TITLE		Direct Submission					

JOURNAL Submitted (14-NOV-1997) Kushnir S., VIB, Dep.Genetics,  
Ledeganckstraat 35, Gent, B9000, Belgium

## FEATURES

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Location/Qualifiers  
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/product="poly(ADP-ribose) polymerase"  
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BASE COUNT 968 a 604 c 813 g 826 t  
ORIGIN

Query Match 100.0%; Score 474; DB 8; Length 3211;  
Best Local Similarity 100.0%; Pred. No. 9.2e-139; Indels 0; Gaps 0;  
Matches 474; Conservative 0; Mismatches 0;

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Qy 61 gggctaagaattgcaactctctgagccctgttactggtctatgttgcgaagcc 120  
Db 2609 GGGCTAAGAAATTGACCTCTCGAGGACCTGTTACTGGCTATATGTTTCGGCAAGGCCTC 2668  
Qy 121 tactttgcagatctagtaagaagagcgacacatactgttattgtgataagaataatcct 180  
Db 2669 TACTTTGCAGATCTAGTAAGAAGAGCGGCAACAATACHTGTTATGTGGATAGGAATAATCCT 2728  
Qy 181 gtagggttgatgctcttcttgaggttctttaggagacatgtatgaactaaagaagcc 240  
Db 2729 GTAGGTTGATGCTCTTTCTGAGGTGCTTTAGGAGACATGTATGAACATAAGAGCC 2788  
Qy 241 acgtccatgagacaaacctccaagaggaagcattcgaccagggattaggcaaaacccgtg 300  
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Qy 361 gtgccatcaatattagagctctgaaactcatgtacaatgagtcacatcgctacaacaca 420  
Db 2909 GTGCCATCATCAATTAGGAGCTCTGAACATCATGTACAATGAGTACATCGTCTACACACA 2968  
Qy 421 tccaggtgagatgcagttcttctgtaaggtgcgtttccatcacagaaggtg 474  
Db 2969 TCCAGGTGAGATGCAGTTCTTCTGCTGAAGGTGCGTTTCCATCACAGAAGGTAG 3022

## RESULT 2

AF093627  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AF093627 3285 bp mRNA PLN 29-NOV-1998  
Zea mays poly(ADP)-ribose polymerase (PARP1) mRNA, complete cds.  
AF093627  
AF093627.1 GI:3928870  
Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 3285)  
Mahajan, P.B. and Zuo, Z.  
Purification and cDNA cloning of maize Poly(ADP)-ribose polymerase  
Plant Physiol. 118 (3), 895-905 (1998)  
99026291  
2 (bases 1 to 3285)  
Mahajan, P.B. and Zuo, Z.  
Direct Submission  
Submitted (22-SEP-1998) Crop Protection, Pioneer HiBred  
International, Inc., 7300 NW 62nd Avenue, Johnston, IA 50131-1004,  
USA

## FEATURES

Source 1...3285  
/organism="Zea mays"  
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/codon\_start=1  
/product="poly(ADP)-ribose polymerase"  
/protein\_id="AAC79704.1"  
/db\_xref="GI:3928871"

## gene

## CDS

## BASE COUNT

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Conservative

## Mismatches

## Indels

## Gaps

## Qy

## Db

## Qy

## Db

## Qy

## Db

## Qy

## Db

## Qy

## Db

## Qy

## Db

## Qy

## Db

## Qy

## Db

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 Db 2749 GTAGGTTTGTATGCTTTCTTCTGAGGTTGCTTTAGGAGACATGTATCACTAAGAAAGCC 2808  
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 Qy 301 ccactgagtcagagttgtgaagtgagggatgtatgctgagttccctgcggcaagccg 360  
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 Db 2929 GTCCCATCATCAATAGGAGCTCTGAACATCATGTACATGATGATCATGCTCATACACACA 2988  
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 Db 2989 TCCAGGTGAAGTCAGTTCTGCTGAAGTGCCTTTCCATCACAAGAGGTAG 3042

RESULT 3  
 ATH131705  
 LOCUS Arabidopsis thaliana mRNA PLN 18-DEC-1998  
 DEFINITION Arabidopsis thaliana mRNA for poly(ADP-ribose) polymerase.  
 ACCESSION AJ131705  
 VERSION AJ131705.1 GI:4038490  
 KEYWORDS NAD(+) ADP-ribosyltransferase; parp-1 gene; poly(ADP-ribose) polymerase.  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 1 (bases 1 to 3187)  
 Direct Submission  
 Submitted (17-DEC-1998) Kazmaier M., Departement D'Ecophysiologie Vegetale Et De Microbiologie, Commissariat A L'energie Atomique, CEA Cadarache, Lab. de Radiobiol. Vegetale, Bat. 185, 13108 St. Paul-les-Durance, FRANCE  
 2 (bases 1 to 3187)  
 Doucet-Chabeaud, G. and Kazmaier, M.  
 Unpublished  
 Location/Qualifiers  
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 /codon\_start=1  
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 /product="poly(ADP-ribose) polymerase"  
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 ORIGIN

mat\_peptide

Query Match 59.18; Score 280; DB 8; Length 3187;  
 Best Local Similarity 74.6%; Pred. No. 2.1e-77;  
 Matches 352; Conservative 0; Mismatches 120; Indels 0; Gaps 0;  
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 Db 2489 AATAAGATGCTCCTATGCGCATGGTTCGATTACGAATTTTGTGGATATTGAACAA 2548  
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 Db 2549 GGACTGAGAATTGCACTCCAGAGCTCTCTACTGTTACATGTTTGGAAAAAGGATA 2608  
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 Qy 241 acgtccatgacaaacctccagagggagcattcgaccagggattagcgaacccgtg 300  
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 Db 2849 GTTTCATCAAGTCAAGCTTCTGAGCTTATGATACATGATATGCTCTACGATACA 2908  
 Qy 421 tccaggtgaagtcagttcttctggaagtgctgttccatcacaagaggt 472  
 Db 2909 GCCCAGGTGAAGTTGCTTCTTGTGAAAGTAAAGGTTTAAAGCACACAGAGAT 2960

RESULT 4  
 RNPARP2  
 LOCUS R.norvegicus mRNA for poly(ADP-ribose) polymerase (clone PRATC).  
 DEFINITION R.norvegicus mRNA for poly(ADP-ribose) polymerase (clone PRATC).  
 ACCESSION X65497  
 VERSION X65497.1 GI:56849  
 KEYWORDS NAD(+) ADP-ribosyltransferase.  
 SOURCE Norway rat.  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 1939)  
 Thibodeau, J., Gradwohl, G., Dumas, C., Clairoux-Moreau, S., Brunet, G., Penning, C., Poirier, G.G. and Moreau, P.  
 Cloning of rodent cDNA coding the poly(ADP-ribose) polymerase catalytic domain and analysis of mRNA levels during the cell cycle  
 Biochem. Cell Biol. 67 (9), 653-660 (1989)

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MEDLINE 90027702
REFERENCE 2 (bases 1 to 1939)
AUTHORS Potvin,F.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-1992) F. Potvin, Molecular Endocrinology, CHUL
Research Center, 2705, Boul Laurier, Ste-Foy, Quebec, G1V 4G2,
CANADA
COMMENT See also X65496.
FEATURES Location/Qualifiers
source 1..1939
/organism="Rattus norvegicus"
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/db_xref="SWISS-PROT:P27008"
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BASE COUNT 524 a 488 c 521 g 426 t
ORIGIN

Query Match 33.5%; Score 158.6; DB 10; Length 1939;
Best Local Similarity 60.1%; Pred. No. 4.8e-39;
Matches 282; Conservative 0; Mismatches 184; Indels 3; Gaps 1;

Qy 1 acaagatgctattatggcaggttcgaagttgacgaatttgggaattcttagtcaa 60
Db 1031 AACCGGAGACTGCTGTGGCAGCGGTCCAGGACCAACCACTTCGACGATCTCTCACAG 1090

Qy 61 gggcctaagaattgcacctctcaggcaacctgttactggtctatatgttcggcaagccctc 120
Db 1091 GGTCTCGGATAGCCCCACCTGAAGCACCTGTGACAGGCTACATGTTTGGGAAGGAATC 1150

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Db 1151 TACTTTGCTGATGGTGTCCAAAGTGCAGAACTACTGCCACAGTCTCAGGAGACCCG 1210

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Qy 241 acgtccatgacaaacctccaaggggaagcattcgaccacgaagggttaggcaaaaccgtg 300
Db 1271 TCTCACATCAGCAAGTTTACCAAGGGGCAAGCAGAGTGTCAAAAGGTTTGGGCAAAACCG-- 1328

Qy 301 ccactggagtcagagtttggagtgaggagtgatgtctgttagtttccctgcggcaagccg 360
Db 1329 -CCCTGACCTTCGGCCACCATCACCTCGATGGTGTGTAGAGGTTCGGCTGGGAACAGG 1387

Qy 361 gtgccatcaatattaggagctctgaactcatgtacatgagtcacatcgtctacaacaca 420
Db 1388 ATTCCGCTCGGTGTATGATACACCTGCTGCTGTATTAACGAGTACATGTGCTACGACATT 1447

Qy 421 tccaggtgaagatgcagttcttgcgaaggtgcgttttccatcacaga 469
Db 1448 GTCAGGTGAATCTGAAGTACCTACTGAAACTGAAGTTCAATTTCAAGA 1496
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## RESULT 5

```
XELPADPRP
LOCUS XELPADPRP 3718 bp mRNA VRT 04-FEB-1999
DEFINITION Frog mRNA for poly(ADP-ribose) polymerase.
ACCESSION D14667
VERSION D14667.1 GI:287584
KEYWORDS poly (ADP-ribose) polymerase.
SOURCE Xenopus laevis egg, oocytes, germ cell, cDNA to mRNA, clone
XPAP5-9R.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 3718)
Uchida,K.
Direct Submission
Submitted (15-MAR-1993) to the DDBJ/EMBL/GenBank databases.
Kazuhiko Uchida, Institute of Basic Medical Sciences, Department of
Biochemistry, Ten-noudai 1-1-1, Tsukuba, Ibaraki 305, Japan
(E-mail:kzuchida@md.tsukuba.ac.jp, Tel:0298-53-3271,
Fax:0298-53-3039)
2 (bases 1 to 3718)
Uchida,K., Uchida,M., Hanai,S., Ozawa,Y., Ami,Y., Kushida,S. and
Miwa,M.
Isolation of the poly(ADP-ribose) polymerase-encoding cDNA from
Xenopus laevis: phylogenetic conservation of the functional domains
Gene 137 (2), 293-297 (1993)
94131300
3 (bases 1 to 3718)
Uchida,K., Uchida,M., Hanai,S., Ishikawa,K., Ozawa,Y., Ueno,N. and
Miwa,M.
Isolation of Poly(ADP-ribose) Polymerase cDNAs from Xenopus laevis
and Cherry Salmon using heterologous oligonucleotide consensus
sequences: gene conservation in amphibia, fish, and insect
Unpublished (1993)
Submitted (15-MAR-1993) to DDBJ by:
Kazuhiko Uchida
Department of Biochemistry
Institute of Basic Medical Sciences
University of Tsukuba
1-1-1 Ten-noudai
Tsukuba, Ibaraki 305
Japan
Phone: 0298-53-3271
Email: kzuchida@md.tsukuba.ac.jp
Fax: 0298-53-3039.
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Matches 278; Conservative 0; Mismatches 179; Indels 3; Gaps 1;

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Qy 69 aattcacctcctcagcagcctgttactgtatgttcgcaaaagccctctacttgc 128
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Qy 129 agatcaggaagagcgcaataactgttattgtgtaggaataatccttaggttt 188
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 Db 3074 CAACCTGAAGTACCTGCTGAAGTCAAGTTCACACTACAAG 3113

RESULT 6  
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 DEFINITION Rattus norvegicus poly(ADP-ribose) polymerase mRNA, complete cds.  
 ACCESSION U94340  
 VERSION U94340.1 GI:2896791  
 KEYWORDS Norway rat.  
 SOURCE Rattus norvegicus  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 3128)  
 Benke S., Meyer R. and Buerkle A.  
 Isolation of cDNA encoding full-length rat (Rattus norvegicus) poly(ADP-ribose) polymerase  
 Biochem. Mol. Biol. Int. 43 (4), 755-761 (1997)  
 98046546

REFERENCE 2 (bases 1 to 3128)  
 Benke S., Meyer R. and Buerkle A.  
 Direct Submission  
 Submitted (18-MAR-1997) Angewandte Tumoriologie, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 242, Heidelberg D-69120, Germany  
 3 (bases 1 to 3128)  
 Benke S., Meyer R. and Buerkle A.  
 Direct Submission  
 Submitted (19-FEB-1998) Angewandte Tumoriologie, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 242, Heidelberg D-69120, Germany

REMARK Sequence update by submitter  
 COMMENT On Feb 19, 1998 this sequence version replaced gi:2583143.  
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BASE COUNT 861 a 758 c 905 g 604 t  
 ORIGIN

Query Match 33.1%; Score 157; DB 10; Length 3128;  
 Best Local Similarity 59.9%; Pred. No. 1-7e-38;  
 Matches 281; Conservative 0; Mismatches 185; Indels 3; Gaps 1;

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 DEFINITION  
 ACCESSION Z12139  
 VERSION Z12139.1 GI:64967  
 KEYWORDS poly(ADP-ribose) polymerase.  
 SOURCE African clawed frog.  
 ORGANISM Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopus.  
 1 (bases 1 to 3617)  
 Saullier-le Drean, B.M.  
 Theses (1992) Lab. de Biol. et Genet. du Developpement, Universite de Rennes 1. URA CNRS 256  
 2 (bases 1 to 3617)  
 Saullier-le Drean, B.M.  
 Direct Submission  
 TITLE Submitted (15-MAY-1992) Saullier-le Drean B.M., Lab. de Biol. et

Genet. du Développement, Université de Rennes I, URA CNRS 256,  
Campus de Beaulieu, Av. du Gal LeClerc, Rennes-cedex, FRANCE, 35042

# FEATURES

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Qy 69 aattgacacctctgagggacactgtactgctatatgttcggcaaaagggcctactcttcg 128  
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Qy 429 gaagatgcagttcttctgctgaaggtgctgtccatcacaa 467  
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## RESULT

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LOCUS 2147 bp mRNA PLN 31-MAY-1995  
DEFINITION A.thaliana PARP mRNA for PARP protein.  
ACCESSION Z48243  
VERSION 248243.1 GI:853721  
KEYWORDS PARP gene; PARP protein.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 2147)  
Lepiniec.L., Babiychuk,E., Kushnir,S., Van Montagu,M. and Inze,D.  
Characterization of an Arabidopsis thaliana cDNA homologue to  
animal poly(ADP-ribose) polymerase  
FEBS Lett. 364 (2), 103-108 (1995)  
95269779  
2 (bases 1 to 2147)  
Lepiniec.L.  
Direct Submission  
Submitted (10-FEB-1995) Lepiniec L., University Gent, Laboratorium  
Genetica, 35 KL Ledeganckstraat, GENT, Belgium, B-9000

## FEATURES

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Best Local Similarity 59.9%; Pred. No. 1.7e-37;
Matches 276; Conservative

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DEFINITION (ADP-ribose) polymerase), clone MGC:6498 IMAGE:2648390, mRNA,
complete cds.
ACCESSION BC012041
VERSION BC012041.1 GI:15080597
KEYWORDS MGC.
SOURCE house mouse.

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DEFINITION	D90073.1	GI:217581			
ACCESSION	D90073				
VERSION					
KEYWORDS	EC 2.4.2.30				
SOURCE	DNA binding protein; helix-turn-helix; nuclear location signal; poly(ADP-ribose) synthetase; zinc-binding finger motif;				
ORGANISM	Bovine thymus, cDNA to mRNA, clone pSO-7.				
	Bos taurus				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
Bovidae; Bovinae; Bos.

1 (bases 1 to 3589)  
Saito, I., Hatakeyama, K., Kido, T., Ohkubo, H., Nakanishi, S., and Ueda, K.

**TITLE** Cloning of a full-length cDNA encoding bovine thymus poly(ADP-ribose) synthetase: evolutionally conserved segments and their potential functions

**JOURNAL** Gene (1990), 100, 1-10

COMMENT  
(1980) in press  
These data kindly submitted in computer readable form by: Isao  
Saito  
Department of Statistics

Department of Clinical Science and Laboratory Medicine Faculty of  
Medicine, Kyoto University  
Shogoinkawahara-cho 54, Sakyo-ku

Kyoto 606  
Japan  
Phone: 075-751-3467

Fax: 075-771-4792  
zinc-binding finger motifs are observed in seq  
The sequences 200-200  
21-51 203 100 100

FEATURES	LOCATION/Qualifiers	SOURCE
sequences, 200-220 and 250-270, showed helix-turn-helix structure. Nucleotide-binding fold was found in seq.	890-903.	

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SNMKILTLGLSSQNKKDEVKATIEKLGGKKLTGTANKASLICISITKEVEVKTALZMPDPL  
ANTRWSEFENRQBZTAKS

SKGPVKEEKTGKSEKRMLTLKGAAVDPSDGLHNAHVLEKGGKVESATLGLVDIVK  
GNSYYKLQLEDDEKSRWYIFFSWGVRGTVI GSNKI FOMCECCH

GNAWSKRMFTTHPKPKFYPLEIDYQDDEEAVKLTVNPQTSKSLPKPVQNLKMFIDVE  
SMKKAMVEYEDIKMPLNGKLSKRQIQAAYSILSEVQALSGSGSDSHLIDLNSREYF  
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LKTDIKVVDKSEAEIIRKYVKNTHTATTHNAYDLEVVDIFKIEREGESQYKPFKQL  
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misc_feature
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/note="nucleotide sequence"

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31.8%; Score 150.6; DR 4.1

Local Similarity	59.1%;	Pred. NO. 1.8e-36;	DB 4;	Length 3589;
ches 277;	Conservative	0;	Mismatches 189;	Indels 3;
				Gaps 1;

I aacaagatgctattatggcacggttcaaggttgacgaatttggggaattcttagtcaa 60



3'UTR  
BASE COUNT 472 a 424 c 493 g 343 t  
ORIGIN  
KCALVEYEDLQKPLGKLSRROIAAAYSLSEVQPVSGSSSESOILDLNRRFTLLI  
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TDIKVVDHSEAEVIRKYVKNTHATNAYDLEVIDIFKIEREGESORYAPFROLHN  
RRLHWSRTTNFAGILSOGRIAPPEAPVTVGFMGKIYFADVMVSYANTCHTSQGD  
PTGLJMLGEVALGNMYELKSHASHISKPKGHSYKGLKTTTDPFSASITLSEVVEPLG  
TGIPSGVNDTCLLYNEYIVYDIAQVNLKLLKLFNFKTSLW"

Query Match 31.4%; Score 149; DB 10; Length 1732;  
Best Local Similarity 58.8%; Pred. No. 5.1e-36;  
Matches 276; Conservative 0; Mismatches 190; Indels 3; Gaps 1;

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Db 1311 GGTCTCGGATAGCCCAACCTGAAGCGCTGTGACAGGCTACATGTTTGGGAAGGATC 1370  
Qy 121 tacttgcagatctagtaagcagagcgcacatactgttattgtgtaggaataatcct 180  
Db 1371 TACTTTGCCACATGGTTCARAAAGTCAAACTACTGCCACACATCTCAGGAGACCCG 1430  
Qy 181 gtagggttgatgcttcttctgaggttcttttaggagacatgtatgaactaagaagcc 240  
Db 1431 ATTGGCTTAATAATGCTGGGAGAGGTTGCCCTTGGAAATATGATGAACATCAAGCATGT 1490  
Qy 241 acgtccatgacaacacctccaagaggagcattccgaccaaaggattaggaacacccgtg 300  
Db 1491 TCATATACAGCAAGTTACCAAGGCAAGCAGACAGTGTCAAGGTTTGGGAAACACC--- 1547  
Qy 301 ccactgagtcagagttgtgaagtggaggtgatgtatgctgtagtccctcgccgaagccg 360  
Db 1548 ACCCTGACCTTCGGCCAGCATCACCTCGAGGGTGTAGAGGTTCCTACTGGGAACAGGG 1607  
Qy 361 gtgccatcaataggagctctgaactcatatgaactgtagtacctatgacatgcttacaaca 420  
Db 1608 ATCCATCTGGTGTCAACAGACACCTGCTGCTGTATTAATAGTACATGTCACGACATT 1667  
Qy 421 tccagtggaagatgcagttcttctgtaaggtgctgtttccatcacaga 469  
Db 1668 GCTCAGGTGAATCTCAATACCTGCTGAACATCAAGTTCATTTTAA 1716

RESULT 15  
AF168781 3047 bp mRNA ROD 28-JUL-1999  
LOCUS  
DEFINITION  
Cricetulus griseus poly ADP-ribose polymerase (PARP) mRNA, complete cds.  
ACCESSION  
AF168781  
VERSION  
AF168781.1 GI:5616519  
KEYWORDS  
Chinese hamster.  
SOURCE  
Cricetulus griseus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.  
REFERENCE  
1 (bases 1 to 3047)  
Ganesh,A.N., Phillips,E., Shah,R., Affar,E.B., Poirer,G., Thacker,J. and Meuth,M.  
Suppression of the radiation sensitive phenotype of hamster irsl and irs2 strains selected for resistance to 3 aminobenzamide  
Unpublished  
2 (bases 1 to 3047)  
Ganesh,A.N. and Meuth,M.  
Direct Submission  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
Ganesh,A.N. and Meuth,M.  
TITLE  
JOURNAL  
Submitted (14-JUL-1999) Oncological Sciences, University of Utah, 15 N. 2030 E., Salt Lake City, UT 84112, USA  
Location/Qualifiers  
FEATURES

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/db\_xref="taxon:10029"  
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1. .3042  
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/protein\_id="A445817.1"  
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TCFVKNREELGFRPEYSASOLKGSLLSAEDKEVLKQLPGVSEKGRKDEVDGAE  
VARKSKGDKSKLEKALKAKQNDLLIWNKDELKACSTSDLEKLLINQOQVPSGE  
SAILDRVADGMAGFALLPKECSQQLVFKSDAYICTGDTAWTKCNKVTGTPSRKEWY  
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VRVCEDFLODVAATSKLOELLASHLSNAEVEVPEVAAPKGSAPSKSGK  
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SYKLQLEDDEKSRMYFRSGRVGTIVIGSNKLEQMPKSEDAVEHEMKLYEKTGNA  
WHSKNFTKPKKFPLEIDYQDEEAVKLTVPKTKLPAKVOELVGHMIFVESHK  
KALVEYEDLQKPLGKLSRROIAAAYSLSEVQPVSGSSSESOILDLNRRFTLLI  
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PTGLJMLGEVALGNMYELKSHASHISKPKGHSYKGLKTTTDPFSASITLSEVVEPLG  
TGIPSGVNDTCLLYNEYIVYDIAQVNLKLLKLFNFKTSLW"

gene

1. .3047

CDS

1. .3042

BASE COUNT

846 a 739 c 869 g 593 t

ORIGIN

Query Match

31.1%; Score 147.4; DB 10; Length 3047;

Best Local Similarity

58.6%; Pred. No. 1.8e-35;

Matches 275; Conservative

0; Mismatches 191; Indels 3; Gaps 1;

Qy 1 aacaagatgctatttgccagcgttcaaggttgacgaatttttgggaatttttagtcaa 60

Db 2563 AATCGGAGGTTACTGTGGCAGCGGTCCAGGACCACTTGTGTGGCATCTCTGTGCACAG 2622

Qy 61 gggctaaagattgcacctcctcctgagcagcctgttactggtctatatgttcggcaagccctc 120

Db 2623 GGTCTCGGATAGCCCAACCTGAAGCAGCCTGTGACAGGCTACATGTTTGGAAAGGATC 2682

Qy 121 tactttgcagatctagtaagcagagcgcacatactgttattgtgtaggaataatcct 180

Db 2683 TATTTTGTGACATGTTGTCAAAAGTGCACAACTACTGCCATACATCTCAGGAGACCCG 2742

Qy 181 gtagggttgatgcttcttctgaggttgccttttaggagacatgtatgaactaagaagcc 240

Db 2743 ATTGGCTTGTACTGTGTGGGAGAGTGCCTTGGAAACATGTACGAACTCAAGCATGCG 2802

Qy 241 acgtccatgacaacacctccaagaggaggaagcattcgcaagggattaggaacaaacccgtg 300

Db 2803 TCACATATACGAAGTTACCAAGGCAAGCAGTGTGTCAAAAGGCTTGGGCAAAAC---G 2859

Qy 301 ccactgagtcagagttgtgaagtggaggtgatgtcgttagtccctcgccgaagccg 360

Db 2860 ACCCTTGACCCCTTCGGCCAGCATCACCTTGAGGGTGTAGAGGTTCCTACTGGGAGGAGG 2919

Qy 361 gtgccatcatcaataggagcctctgaactcatgtacaatgtagtacctgtctacacacaga 420

Db 2920 ATCCCATCGGGTGTAAATGACACCTTCCTACTATATAACGAGGTACATCTCTATGACATT 2979

Qy 421 tccagtggaagatgcagttcttctgtaaggtgctgtttccatcacaga 469

Db 2980 GCTCAGGTGAACCTGAATACCTGCTGAAACTGAAGTTTAAATTTTAA 3028



Fri Mar 8 08:32:02 2002

Search completed: March 7, 2002, 16:49:01  
Job time: 8171 sec

us-09-236-995d-3.rge

Page 12

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2002, 18:16:17 ; Search time 298.35 Seconds  
(without alignments)  
1362.065 Million cell updates/sec

Title: US-09-236-995D-3

Perfect score: 474

Sequence: 1 aacagatgctattatggca.....gtttccatcacagaggttag 474

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID22/gcgdata/geneseq/geneseq/NA1981.DAT.\*  
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22: /SID22/gcgdata/geneseq/geneseq/NA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	ID	Description
1	474	100.0	2949	20	AA89542	Maize poly ADP-rib
2	474	100.0	3211	21	AAZ60615	DNA encoding the p
3	474	100.0	3212	21	AAZ60618	DNA encoding the p
4	154.4	32.6	2147	21	AAZ60617	DNA encoding the p
5	151.4	31.9	2295	21	AAZ60616	DNA encoding the p
6	142.6	30.1	3580	20	AAZ23799	Human poly(ADP-rib
7	142.6	30.1	3793	17	AAT13732	DNA-binding domain
8	139.4	29.4	3045	22	AAT63954	Human tankyrase2 r
9	137.8	29.1	5345	16	AAT04221	5.3 kb EcoRI fragm
10	136.2	28.7	2682	16	AAT04219	Poly(ADP-ribose)-p
11	122.6	25.9	864	22	AA85320	3' end fragment of

Human poly(ADP-rib  
hparp2 cDNA. Homo  
Human brain PARP2  
Human brain poly-A  
Human ORF ORF2673  
Fusion protein PAR  
Human cDNA sequenc  
Human colon cancer  
Poly(ADP-ribose)-p  
Enterococcus faeca  
Human brain PARP3  
Human uterus type  
Probe #9163 used t  
NAD(+) ADP-ribosyl  
EST AA568817, frag  
Colon tumour relat  
H. pylori GHPO 150  
Human cDNA clone (c  
Human secreted pro  
Aspergillus oryzae  
Codon-optimised mu  
Shrimp white spot  
Arabidopsis thalia  
ACNPV ORF 54, resi  
Drosophila morphog  
Drosophila morphog  
Drosophila morphog  
ACNPV genomic DNA  
Human gene signatu  
Human secreted pro  
Human secreted pro  
Codon-optimised HP  
Stromelysin gene c

#### ALIGNMENTS

RESULT 1

AA89542

ID AAX89542 standard; cDNA; 2949 BP.

XX AC AAX89542;

DT 06-OCT-1999 (first entry)

XX DE Maize poly ADP-ribose polymerase gene.

DE PARP; poly ADP-ribose polymerase; metabolism; maize; transform; ss.

XX Zea mays.

XX Key Location/Qualifiers

FT CDS 1..2949

FT /product= "PARP"

FT /transl\_except= (pos:1453..1455, aa:Xaa)

FT /transl\_except= (pos:1495..1497, aa:Xaa)

FT /transl\_except= (pos:1504..1506, aa:Xaa)

FT /transl\_except= (pos:1534..1536, aa:Xaa)

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FT /transl\_except= (pos:1582..1584, aa:Xaa)

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FT /transl\_except= (pos:1594..1596, aa:Xaa)

FT /transl\_except= (pos:1975..1977, aa:Xaa)

FT /transl\_except= (pos:2011..2013, aa:Xaa)

FT /transl\_except= (pos:2014..2016, aa:Xaa)

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FT /transl\_except= (pos:2047..2049, aa:Xaa)

FT /transl\_except= (pos:2050..2052, aa:Xaa)

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61	QY	61	gggctaagaattgcacctctctgaggcacctgttactggctatatgttcggcacaaggcctc	120
2536	Db	2536	gggctaagaattgcacctctctgaggcacctgttactggctatatgttcggcacaaggcctc	2595
121	QY	121	tactttgcagatcttagtaagcaagacgcacaaactctgttatgttcggataggaaataaactct	180
2596	Db	2596	tactttgcagatcttagtaagcaagacgcacaaactctgttatgttcggataggaaataaactct	2655
181	QY	181	gtaggtttgatgctctcttctgaggtgtcttttaggagacatgatatgaactaaagaagacc	240
2656	Db	2656	gtaggtttgatgctctcttctgaggtgtcttttaggagacatgatatgaactaaagaagacc	2715
241	QY	241	acgtccatggacaaacctccaaggagggaagcattcgaccaagggataggcaaaacccgtg	300
2716	Db	2716	acgtccatggacaaacctccaaggagggaagcattcgaccaagggataggcaaaacccgtg	2775
301	QY	301	ccactggagtcagagtttctgaaagtcggaggatgatctgtagtctccctgcggcaaacccg	360



NAP; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase;  
 KW programmed cell death; apoptosis; growth rate; stress; cold; pathogen;  
 KW pest; drought; heat; fungi; nematode; seed-shatter; ss.  
 XX  
 OS *Arabidopsis thaliana*.

Key	Location/Qualifiers
CDS	129..2042
	/*tag= a
	/product= "NAP protein"

WO200004173-A1.

27-JAN-2000.

12-JUL-1999; 99WO-EP04940.

17-JUL-1998; 98US-0118276.

(PLBZ ) PLANT GENETIC SYSTEMS NV.

Babiychuk E, Kushnir S, De Block M:

WPI; 2000-182436/16.

P-PSDB; AAY68835.

Modulating cell death, growth and stress resistance in eukaryotes, specifically plants, used, e.g. to impart fungus or nematode resistance

Disclosure: Page 95-99: 126pp: English.

The present sequence encodes a NAP protein. This protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The NAP polynucleotide sequences can be used for modulation of programmed cell death in eukaryotic cells. The method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. Reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc., or during transformation). Particular applications are generation of plants that are resistant to fungi or nematodes; are male or female sterile; or have better seed-shatter properties. The methods are also used to improve growth of transformed plant cells (and derived calli or complete plants).

Sequence 2147 BP; 704 A; 393 C; 496 G; 554 T; 0 other:

Query Match 32.6%; Score 154.4; DB 21; Length 2147;  
Best Local Similarity 59.2%; Pred. No. 2.1e-41;  
Matches 282; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

QY	1	aacaaagatgctattatagcagcgggtccaaaggttgacgaatttttgaggaaattcttagtcoa	60
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QY	61	gggctaaagaattgcactcctctggagcaccgttactcggcttatatgttcggcaaggcctc	120
Db	1626	ggctcgcgaatagctcctctctgaagcgccctgttaactcggttcacatgtttggaaaaggggct	1685
QY	121	tactttgcagatctagtaagcaagcgcacatactgttatgtgataggaaataatcct	180
Db	1686	tactttgcggatagtgtctccaaagtcgcgaactattgctatgccaaactgcgcgctaata	1745
QY	181	qtaggatttgatgcctctttctgaagttgcctcttaggagacatgtatgaactaaagaa---	237
Db	1746	gatggcggtctgcctctcgcaggttcgctttgggagacaatgaatgaactctgttatcca	1805
QY	238	gccagctccatggacaaacctccaaagggaagcaatctaccacgaagggttaggcacaaacc	297



XX DNA-binding domain of poly(ADP-ribose) polymerase coding sequence.  
 XX PARG; DNA-binding domain; poly(ADP-ribose) polymerase; gene therapy;  
 KW tumour treatment; DNA repair; over-expression; ss.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 96..3137  
 FT /\*tag= a  
 FT /product= poly(ADP-ribose)\_polymerase  
 FT /note= "PARG"  
 FT 67..1220  
 FT /\*tag= b  
 FT /note= "encodes DNA-binding domain"  
 XX  
 FT W09618737-A2.  
 PN  
 XX 20-JUN-1996.  
 PD  
 XX 15-DEC-1995; 95WO-DE01817.  
 XX  
 XX 16-DEC-1994; 94DE-444949.  
 PR  
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 XX Buerkle A, Kuepper J, Zur Hausen H;  
 PI  
 XX WPI; 1996-300654/30.  
 DR  
 DR P-PSDB; AAR99642.  
 XX  
 XX Vectors contg. insert encoding DNA-binding domain of  
 PT poly(ADP-ribose) polymerase - useful for gene therapy, esp. of  
 PT tumours  
 XX  
 XX Claim 4; Fig 1; 22pp; German.  
 XX  
 XX The present sequence encodes a poly(ADP-ribose) polymerase (PARG) contg.  
 CC a DNA-binding domain (DBD). The DNA fragment from -29 to +1127  
 CC (nucleotides 67-1220 of this sequence) encoding the DBD can be inserted  
 CC into vectors which are used for gene therapy. Over-expression of the DBD  
 CC inhibits the DNA repair function of PARG, so the vectors are useful for  
 CC gene therapy or tumours, esp. in combination with conventional chemo-  
 CC and/or radiotherapy.  
 XX  
 XX Sequence 3793 BP; 1049 A; 847 C; 1034 G; 863 T; 0 other;

Query Match 30.1%; Score 142.6; DB 17; Length 3793;  
 Best Local Similarity 58.0%; Pred. No. 2.5e-37;  
 Matches 272; Conservative 0; Mismatches 194; Indels 3; Gaps 1;  
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 DB 2658 aaccgaagattgctgtgacgggtccaggaccacaaactttgctggatcctgtcccag 2717  
 QY 61 gggcctaagaattgcacctctgagccactgttactggtatattgttcgcaagcctc 120  
 DB 2718 ggtctcgatagcccgctgaagcgcctgtgacgggtacatgtttgtgaaaggatc 2777  
 QY 121 tactttcagatctagtaagcaagagcgacatactgttattgtgataaggaataatcct 180  
 DB 2778 tatttcgctacatggtctccaagagtgccaaactactgcatcgtctcaggagaccga 2837  
 QY 181 gtagggttgatgctcttcttctgaggttgcttttagggagacatgtatgaactaagaagcc 240  
 DB 2838 ataggcttaactcctgttgggagaagttgccccttggaacatgtatgaactgaagcagct 2897  
 QY 241 acgtccatggacaaacctccaagggagcattcgcaccaagggattagggcaaacgctg 300  
 DB 2898 tcacatacagcaagttaaccacaaaggcgcaagcagctgtcacaagggtttgggcaaacctacc 2957

QY 301 ccactggagtcagagtttgtgaagtggaggatgatgctagttccctgcggcaagcgg 360  
 DB 2958 ctgataccttcag---ctaacattagctctggatgggtgtagacgttccctcttgggaccggg 3014  
 QY 361 gtccatcatcaataggagcctctgaactcatgtacaaatgagtagacatcgtctacaacaca 420  
 DB 3015 attcatcgtggtgaatgacacctctctactataacagtagatattgtctatgatatt 3074  
 QY 421 tccagggtgaagatgcagttctgtgctgaaggtgcgtttccatcaacaaga 469  
 DB 3075 gctcaggtaaatctgaagtatctgctgaaactgaaattcaattttaaga 3123

## RESULT 8

AAF63954  
 ID AAF63954 standard; DNA; 3045 BP.

XX AAF63954;

XX DT 05-APR-2001 (first entry)

XX Human tankyrase2 related coding sequence SEQ ID NO: 136.

XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;  
 KW inflammatory disorder; ds.

XX Homo sapiens.

XX WO200100849-A1.

XX PD 04-JAN-2001.

XX PF 28-JUN-2000; 2000WO-US17827.

XX PR 29-JUN-1999; 99US-0141582.

XX PA (ICOS-) ICOS CORP.

XX PI Christenson E, Demaggio AJ, Goldman PS, McElligott DL;

XX DR WPI; 2001-102896/11.

XX DR P-PSDB; AAB66296.

XX New tankyrase2 polypeptides, useful for treating conditions mediated by  
 PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,  
 PT inflammatory and autoimmune disorders -

XX Example 2; Page 203-207; 242pp; English.

XX The present invention provides the protein and coding sequence for the  
 CC human tankyrase2 protein. This is found in two different versions,  
 CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has  
 CC polyADP-ribosylation activity and is involved in the modification of  
 CC TRF1, which is a telomere-specific binding protein. The regulation of  
 CC telomere length, in which TRF1 has a role, is linked to ageing and  
 CC cancer. The sequences are useful in the treatment of cancers and  
 CC inflammatory disorders.

XX Sequence 3045 BP; 863 A; 710 C; 851 G; 621 T; 0 other;

Query Match 29.4%; Score 139.4; DB 22; Length 3045;  
 Best Local Similarity 57.6%; Pred. No. 2.7e-36;  
 Matches 270; Conservative 0; Mismatches 196; Indels 3; Gaps 1;

QY 1 aacaagatgctattatggcagcgttcaaggttgacgaattttgtgggaattcttagtcaa 60  
 DB 2566 aaccgaagattgctgtgacgggtccaggaccacaaactttgctggatcctgtcccag 2625  
 QY 61 gggcctaagaattgcacctctcctcaggcactgttactgctatattgttcgcaagcctc 120  
 DB 2626 ggtcttcgtagcccccgcctgaagcgcctgtgacaggctacatgtttgtgaaaggatc 2685



121	QY	tacttgcagatctagtaagcaagagcgacaaatactgttatgtgtgagtaggaataacct	180
2686	Db	tatttcgtgacatggtctccaagagtcgcaactactaccatactcgtctcaggagagacca	2745
181	QY	gtaggtttgagctcttcttctgaggttgcctttaggagacatgtatgaactaaagaaagcc	240
2746	Db	ataggcttaatccgtgtgggagaagttgccttggaaacatgtatgaactgaagcagct	2805
241	QY	aagtcacatggacaacctccaagagggaagcattcgaccaaaggtattagcaaaacccgtg	300
2806	Db	tcacatatcagcaggttaccacaagggcaagcacagctgtcacaaggtttgggcaaaaatacc	2865
301	QY	ccactggagtcagagtttgtgaagtggaggagatgatgtctgattctcccgcggcaagcgg	360
2866	Db	cctgactctcag--ctaacattagctggatgggtgtagacgttctctcttgggacccggg	2922
361	QY	gtgcacatcaaataggagctgtgaactcatgtacaaatgatacatcgtctacaacaca	420
2923	Db	atttcactgtgtgatagacacctctctactataaacgagtcacattgctatgatatt	2982
421	QY	tcccagggtgaagatgcagttcttctgaaagtgcggttccatcacaga	469
2983	Db	gtcagcgaataatcttgaatattctctctaaactgaacttcaattttaaaga	3031

RESULT	9
AAT04221	
ID	AAT04221 standard; DNA; 5345 BP.
XX	
XX	
AC	AAT04221;
AC	
XX	
XX	
DT	31-MAR-1996 (first entry)
DE	
XX	5.3 kb ECORI fragment containing poly(ADP-ribose)-polymerase gene.

DNA primer; PCR; polymerase chain reaction;  
poly(ADP-ribose)-polymerase; cancer diagnosis; chromosome-13;  
pseudogene; Burkitt's lymphoma; B-follicular cell lymphoma;  
small cell lung carcinoma; colorectal carcinoma; tumor;  
breast carcinoma.

yy Homo sapiens.

US5449605-A.

XX  
PD 12-SEP-1995.

AA  
PF 14-OCT-1988; 88US-0257696.

XX  
PR 06-APR-1993; 93US-0044618.

PR 14-OCT-1988; 8805-025/696.  
XX

XX  
PA (GEOU ) UNIV GEORGETOWN.XX  
PT Cherney B, Lyn D, Smulson ME;

XX DB WPT: 1995-327692/42.

XX Allele-specific primers for detecting pre-disposition to cancer -  
PT caused by a deletion in chromosome 13  
PT (ADP-ribose) polymerase  
PT pseudo-gene for poly

XX  
PS Disclosure: Page 41-46: 47pp: English.

CC This sequence corresponds to a 5.3 kb EcoRI fragment that contains  
CC the poly(ADP-ribose)-polymerase pseudogene.  
XX

XX sequence 5345 BP: 1598 A; 1142 C; 1396 G; 1209 T; 0 other;  
S0

Query Match	29.1%	Score 137.8;	DB 16;	Length 5345;
Best Local Similarity	57.4%;	Pred. No. 1.2e-35;		
Matches 269;	Conservative	0;	Mismatches 197;	Indels 3; Gaps 1;

QY	1	aacaagatgctattatggcgcaggttcaaggctgacgaattttgtgggaatttccttagtcaa	60
Dbb	3519	aactgaaggttgctgtgtgcatgggtccagagaccaccaaatcttgtctgggatctgtcccctg	3578
QY	61	gggtcaagaattgcacctctctggagcacctgttactggctatatgttctggccaagacctc	120
Dbb	3579	ggctcttgatagccccgctcgaaagcacctgtgatgggtacatgttgggttaagtgtac	3638
QY	121	tactttgcagatctagtaaagcaagagcgacataactgttatgttgataggaaataactc	180
Dbb	3639	tatttcgctgactctgtctccagagtgccaaagcactgccatacatcttaggaagaccoca	3698
QY	181	gtaggtttgatgctcttcttgagttgcttttagggagacatgtatgaacttaagaaaagcc	240
Dbb	3699	atagggtaatactctgtcgggaagaagtttgcccttggaaaactgtgtgaactgaagcatgct	3758
QY	241	acgtccatggacaaacctcccaagagggaagcaattcgaccaagggtataggcaaaacctgtg	300
Dbb	3759	tcacataatcagaagtatacccaaggccaagcacagtgtcgaaggtttgggcaaaactact	3818
QY	301	ccactggagtcagagatttgtgaagtggagggatgattctgaattccctgcgcgaagccg	360
Dbb	3819	cctgaaccttcag---ctagtatccactggatgggtgtagaggttccctcttggaccagg	3875
QY	361	gtgccatcatcaattaggagctctgaactcatgtcacatgacatgtacatctgtctacaacaca	420
Dbb	3876	gttctcatctggtgtgaatgacacctgtcactgtataatgagtacattgtctatgatatt	3935
QY	421	tcccaggttgaagatgcagttctctgtcgaagtcgctgttccatcacaga	469
b	3936	gtccaggttaaacctcgaatatctctggaactggaattcaattcaattttaa	3984

RESULT	10
--------	----

RECEIVED  
AAT04219

ID AAT04219 standard; DNA; 2682 BP.

AA  
AC AAT04219;

XX	31-MAR-1996 (first entry)
DT	

XX  
DE  
XX  
poly(ADP-ribose)-polymerase alpha-allele DNA from chromosome-13.

XX  
XV DNA primer:  
XX PCR polymerase chain reaction:

kw DNA primer; PCR; polymerase chain reaction;  
zf poly(ADP-ribose)-polymerase: cancer diagnosis; chromosome-13;

KW poly(ADP-ribose)-polymerase; cancer diagnosis; chromosome  
KW pseudogene: Burkitt's lymphoma; B-follicular cell lymphoma;

KW pseudogland; Burkitt's lymphoma; B cell; carcinoma; tumor;  
KW small cell lung carcinoma; colorectal carcinoma; tumor;

KW small cell lung carcinoma  
KW breast carcinoma: ss.

XX Homo sapiens.

XX  
DN  
RICEA10605-AXX  
13-SEP-1995XX  
14 00E 1000 0000-0257606XX  
01571700 2420 000 6-1-82

PR 06-APR-1993; 93US-0044618.  
PR 06-APR-1993; 93US-0044618.  
PR 06-APR-1993; 93US-0044618.

XX

XX  
XX

XX

Allele-specific primers for detecting pre-disposition to cancer caused by a deletion in chromosome 13 pseudo-gene for poly

XX

XX 22

CC This sequence is of the poly(ADP-ribose)-polymerase alpha-allele.  
 CC A DNA primer specific to this sequence may be used in a PCR  
 CC amplification method to differentiate between the alpha- and beta-  
 CC alleles of the processed pseudogene.  
 XX  
 SQ Sequence 2682 BP; 772 A; 618 C; 711 G; 581 T; 0 other;

Query Match 28.7%; Score 136.2; DB 16; Length 2682;  
 Best Local Similarity 57.1%; Pred. No. 3e-35;  
 Matches 268; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

QY 1 aacagatgctattatggcagcgttcaaggttgacgaatttgggaatttttagtcaa 60  
 DB 2050 aactgaaggttgctgtggtccagcagcaccacacttggcgtccctcgt 2109  
 QY 61 gggcgaagattgacactcctgagcagcctgttactggttatgttcggcaaaagccctc 120  
 DB 2110 ggtcttgtagcagcctgctgaagcaccctgtagggcctacatgttggtaagtgatc 2169  
 QY 121 tacttgcagatctagtaagcagagcgcacataactgttattgttgatagggaataatcct 180  
 DB 2170 tatttcgctgatttctctccagagtgccacgactgcacatactttaggaagaccoca 2229  
 QY 181 gtagggttgccttcttctgaggttgctttagagacatgtatgaactaaagaaagcc 240  
 DB 2230 atagggttgccttctggaagagtgcccttggaacgtgtggaactgaagcatgct 2289  
 QY 241 acgtccatgagcaaacctccagaggaagcattcgacacaggttaggcaaaacccgtg 300  
 DB 2290 tcacatcagcaagttacccaagggcagcagcagtgatcaaggttggcgaactact 2349  
 QY 301 ccactggaagtcaggttggtagtgagggtgagtgctgtagtccctgcggcaagcgc 360  
 DB 2350 cctgacacttccag---ctagatccacactgtaggtgtagaggttccctcgggaccagg 2406  
 QY 361 gtgcatcatcaattaggagctctgaactcagtcacatgtagtgcacatgctacacaca 420  
 DB 2407 gttcatctggtgtagaagcactctctactgttataatgtagtactgtctatgatt 2466  
 QY 421 tccagggtgaagatcagctcttctgtagaggtggtggttcccatcaaga 469  
 DB 2467 gctcaggtaaatctgaatatctctgtagaactgaactgaattcaattttaaga 2515

RESULT 11  
 AAC85320  
 ID AAC85320 standard; cDNA; 864 BP.  
 AC AAC85320;  
 XX  
 XX  
 XX 29-MAR-2001 (first entry)  
 XX  
 DE 3' end fragment of hparp2, 3'-hparp2.  
 XX  
 XX Human; poly(ADP-ribose) polymerase; hparp2; oxidative stress; ARDS;  
 KW inflammation; ischemic stroke; hemorrhagic shock; myocardial ischemia;  
 KW infarction; cerebral vasospasm; rheumatoid arthritis; osteoarthritis;  
 KW gouty arthritis; spondylitis; Behcet's disease; sepsis; septic shock;  
 KW endotoxic shock; gram negative sepsis; gram positive sepsis; trauma;  
 KW toxic shock syndrome; multiple organ injury syndrome; vasculitis;  
 KW hemorrhage; conjunctivitis; uveitis; thyroid-associated ophthalmopathy;  
 KW eosinophilic granuloma; asthma; chronic bronchitis; allergic rhinitis;  
 KW chronic obstructive pulmonary disease; silicosis; reperfusion injury;  
 KW pulmonary sarcoidosis; pleurisy; alveolitis; pneumonia; myocardium;  
 KW scar tissue formation; pulmonary oxygen toxicity; keloid formation; brain;  
 KW autoimmune thyroiditis; multiple sclerosis; systemic lupus erythematosus;  
 KW graft versus host disease; allograft rejection; cystic fibrosis;  
 KW Crohn's disease; ulcerative colitis; inflammatory bowel disease;  
 KW inflammatory dermatitis; contact dermatitis; atopic dermatitis;  
 KW psoriasis; urticaria; fever; myalgia; meningitis; encephalitis;

KW Sjogren's syndrome; alcoholic hepatitis; bacterial pneumonia;  
 KW hypovolemic shock; Type 1 diabetes mellitus; hypersensitivity;  
 KW leukocyte dyscrasia; thermal injury; cytokine-induced toxicity;  
 KW expressed sequence tag; EST; RACE; PCR; amplify; primer;  
 KW polymerase chain reaction; ds.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 1..864  
 FT /\*tag= a  
 FT /product= "hPARP2 C-terminal fragment"  
 FT  
 FT W0200077179-A2.  
 PN 21-DEC-2000.  
 PD 16-JUN-2000; 2000WO-US16629.  
 XX 16-JUN-1999; 99US-0139543.  
 XX (ICOS-) ICOS CORP.  
 XX Christenson E, Demaggio AJ, Goldman PS, McElligott DL;  
 WPI: 2001-025335/03.  
 DR P-PSDB; AAB47031.  
 XX  
 XX New human poly(ADP-ribose) polymerase for treating inflammatory,  
 PT neurological, cardiovascular, or neoplastic tissue growth disorders,  
 PT such as, arthritis, encephalitis, myocardial ischemia, and leukocyte  
 PT metastasis  
 XX  
 XX Example 2; Page 101; 129pp; English.  
 XX  
 CC This sequence represents the 3' fragment of the human parp2  
 CC (poly(ADP-ribose) polymerase) cDNA. This sequence was amplified  
 CC using the primers given in AAC85315-17. DNA derived from a testis  
 CC cDNA library was used as a template. The protein of the invention,  
 CC hPARP2, causes the covalent addition of polymers of ADP-ribose to  
 CC protein targets. hPARP2 activity is induced in many instances of  
 CC oxidative stress or during inflammation where there is direct  
 CC damage to the DNA. hPARP2 may be used to identify antagonists  
 CC which may be used to treat a human having a disorder mediated by  
 CC PARP2 activity, such as, inflammatory, neurological, cardiovascular,  
 CC or neoplastic tissue growth disorders. hPARP2 and antibodies to it,  
 CC can also be used to diagnose these conditions.  
 XX  
 SQ Sequence 864 BP; 250 A; 207 C; 193 G; 214 T; 0 other;

Query Match 25.9%; Score 122.6; DB 22; Length 864;  
 Best Local Similarity 56.9%; Pred. No. 6.2e-31;  
 Matches 268; Conservative 0; Mismatches 194; Indels 9; Gaps 2;

QY 1 aacagatgctattatggcagcgttcaaggttgacgaatttgggaattttagtcaa 60  
 DB 376 aacagatgcttctatggcatgttccagatgagtaactgggtgggaattcttagagccat 435  
 QY 61 gggcgaagattgacactcctgagcagcctgttactggtctatgttcggcaaaagccctc 120  
 DB 436 gggcctcgaattggccaccactgaagctcccatcacaggttacctgtttgggaaggaatc 495  
 QY 121 tacttgcagatcttagtaagcagcagcagcacaactcttatgttgataggaaataatcct 180  
 DB 496 tacttgcagatcttctcccaagagtgcccaactactcttctgctcctcgcctaaagaaat 555  
 QY 181 gtagggttgccttcttctgtgaggttctttaggagacatgtatgaactaaagaaagcc 240  
 DB 556 acaggactgctgctctctatcagaggtagctcttagtgcagtgtaataactactagagcc 615  
 QY 241 acgtccatgagcaaa---acctcccaagaggggaagccttcgacacagggattaggcaaaccc 297

Db 616 aatcctaagccgaaggattgcttcaaggtaaacatagcaccacgaagggtgggaagatg 675  
 Qy 298 gtccactgagtcagagattg-----tgaagtgaaggatgatgctagttccctgc 351  
 Db 676 gtccactgagtcagagattg-----tgaagtgaaggatgatgctagttccctgc 735  
 Qy 352 ggaagcgggtgcatcatcaatagagctctgaactcatgtacacatgacatgacatgc 411  
 Db 736 agtgacacagaattctgaatccagatggttatacctcaactacaatgaatatgtga 795  
 Qy 412 tacaacacatccacagtggaagtgagctctgtgctgaagtgagctgttccat 462  
 Db 796 tataaccccacaggtccgctgtagctgctaccttttaaggttcagttta 846

## RESULT 12

AAF59996  
 ID AAF59996 standard; cDNA; 1566 BP.

XX AAF59996;

XX 11-MAY-2001 (first entry)

XX Human poly(ADP-ribose) synthetase shbPARS2 cDNA.

XX Human; poly(ADP-ribose) synthetase; shbPARS2; vaccine; drug screening;  
 KW ischaemic disorder; cerebral ischaemia; cardiac ischaemia;  
 KW myocardial infarction; stroke; inflammation; autoimmune disease;  
 KW diabetes; multiple sclerosis; neurodegenerative disease;  
 KW Parkinson's disease; Alzheimer's disease; chromosome localisation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 XX CDS 1..1566

XX /\*tag= a  
 XX /product= "Human poly(ADP-ribose) synthetase shbPARS2"

XX WO200112645-A1.

XX 22-FEB-2001.

XX 10-AUG-2000; 2000WO-US21775.

XX 12-AUG-1999; 99US-0373441.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX Barone F, Field J, Kabnick KS, Li X, McQueney MS, Zhu Y;

XX WPT: 2001-211196/21.

XX P-PSDB; AAB60693.

XX New human polypeptide of the polyADPribose synthetase family for use in  
 PT diagnostic assays and for screening modulators used for preventing and  
 PT treating inflammation, autoimmune disease and Alzheimers disease

XX Claim 2; Page 21; 30pp; English.

XX This sequence represents cDNA encoding a novel human poly(ADP-ribose)  
 CC synthetase, shbPARS2. The invention also relates to fragments,  
 CC variants and sequences with at least 95% identity to the shbPARS2  
 CC protein or nucleotide sequence; expression systems and host cells  
 CC comprising an shbPARS2 nucleic acid sequence; The recombinant expression  
 CC of shbPARS2; and an antibody specific for shbPARS2. shbPARS2 proteins  
 CC and nucleotides are useful as vaccines for inducing an immunological  
 CC response in a mammal. The shbPARS2 protein is useful for identifying  
 CC compounds which inhibit or stimulate its activity or expression level.  
 CC Such agonists and antagonists of shbPARS2 are useful for treating human  
 CC diseases including ischaemia and ischaemic tissue injury (e.g., cerebral  
 CC and cardiac ischaemia, myocardial infarction, stroke), inflammation,  
 CC autoimmune disease (e.g., diabetes, multiple sclerosis) and  
 CC neurodegenerative diseases (e.g., Parkinson's disease and Alzheimer's

CC disease). shbPARS2 nucleic acids are useful as diagnostic reagents for  
 CC detecting mutations in the associated gene; as hybridisation probes;  
 CC to isolate full-length shbPARS2 cDNAs and shbPARS2 genomic clones; and  
 CC as an immunogen to produce antibodies for therapeutic use. shbPARS2  
 CC proteins, nucleotides and antibodies are also useful in screening methods  
 CC for detecting the effect of added compounds on the production of mRNA and  
 CC protein in cells.

XX Sequence 1566 BP; 490 A; 328 C; 381 G; 367 T; 0 other;

Query Match 25.9%; Score 122.6; DB 22; Length 1566;  
 Best Local Similarity 56.9%; Pred. No. 8.3e-31;  
 Matches 268; Conservative 0; Mismatches 194; Indels 9; Gaps 2;

Qy 1 aacaagatgctattatggcacggtttcaaggttgacgaattttgtgggaattcttagtcaa 60  
 Db 1078 aacaggatgcttctatggttgcatggttccaggatgagtaactggtgggaattcttagtcaa 1137  
 Qy 61 gggctaaagaattgcaoctctctgagcactgcttactggtctatatgttcggcaaaagcctc 120  
 Db 1138 gggcttcaattgcccacactgaagctcccatcacaggttacatgtttgggaaggaatc 1197  
 Qy 121 tactttgacatctagtaagcaagcgcacaaactactgttattgtgtaggaataactct 180  
 Db 1198 tactttgacatctcttcccaagagtgccaattactgcttctgctctgcctaaagaat 1257  
 Qy 181 gtaggtttgatgcttcttctgaggttctttaggagacatgtatgaactaaagaagcc 240  
 Db 1258 acaggactgctcttctatcacaggtagctctgagtcagtgtaagtaactactagggcc 1317  
 Qy 241 acgtccatgacaaa---acctcaagagggaagcattcgcacaaagagattagcacaacc 297  
 Db 1318 aatcctaaggcgaaggattgcttcaaggtaaacatagcaccacgaagggtggcaagatg 1377  
 Qy 298 gtccactgagtcagagtttg-----tgaagtgaaggatgatgctagttccctgc 351  
 Db 1378 gtccactgagtcagagtttg-----tgaagtgaaggatgatgctagttccctgc 351  
 Qy 352 ggaagcgggtgcatcatcaatagagctctgacactcatgtacacatgacatgacatgc 411  
 Db 1438 agtgacacaggaattctgaatccagatggttatacctcaactacaatgaatatgtga 1497  
 Qy 412 tacaacacatccacagtggaagtgagctctgctgagagtgaggttcggttccat 462  
 Db 1498 tataaccccacaggtccgctgtagctgctaccttttaaggttcagttta 1548

## RESULT 13

AAC85303  
 ID AAC85303 standard; cDNA; 1814 BP.

XX AAC85303;

XX 29-MAR-2001 (first entry)

XX hparp2 cDNA.

XX Human; poly(ADP-ribose) polymerase; hPARP2; oxidative stress; ARDS;  
 KW inflammation; ischaemic stroke; hemorrhagic shock; myocardial ischemia;  
 KW infarction; cerebral vasospasm; rheumatoid arthritis; osteoarthritis;  
 KW gouty arthritis; spondylitis; Behcet's disease; sepsis; septic shock;  
 KW endotoxic shock; gram negative sepsis; gram positive sepsis; trauma;  
 KW toxic shock syndrome; multiple organ injury syndrome; vasculitis;  
 KW hemorrhage; conjunctivitis; uveitis; thyroid-associated ophthalmopathy;  
 KW eosinophilic granuloma; asthma; chronic bronchitis; allergic rhinitis;  
 KW chronic obstructive pulmonary disease; silicosis; reperfusion injury;  
 KW pulmonary sarcoidosis; pleurisy; alveolitis; pneumonia; myocardium;  
 KW bronchiectasis; pulmonary oxygen toxicity; keloid formation; brain;  
 KW scar tissue formation; atherosclerosis; systemic lupus erythematosus;  
 KW autoimmune thyroiditis; multiple sclerosis; Reynaud's syndrome;  
 KW graft versus host disease; allograft rejection; cystic fibrosis;

KW chronic glomerulonephritis; inflammatory bowel disease;  
 KW Crohn's disease; ulcerative colitis; necrotizing enterocolitis;  
 KW inflammatory dermatosis; contact dermatitis; atopic dermatitis;  
 KW psoriasis; urticaria; fever; myalgia; meningitis; encephalitis;  
 KW Sjogren's syndrome; alcoholic hepatitis; bacterial pneumonia;  
 KW hypovolemic shock; type 1 diabetes mellitus; hypersensitivity;  
 KW leukocyte dyscrasia; thermal injury; cytokine-induced toxicity; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 63..1814  
 FT /\*tag= a  
 FT /product= "hPARP2"

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Sequence 1814 BP; 558 A; 389 C; 462 G; 405 T; 0 other;

Query Match 25.9%; Score 122.6; DB 22; Length 1814;  
 Best Local Similarity 56.9%; Pred. No. 9e-31;  
 Matches 268; Conservative 0; Mismatches 194; Indels 9; Gaps 2;

QY 1 acaagatgctattatgacgaggttcaaggttgacgaatttttgggaattcttagtcaa 60

Db 1326 aacaggtatgcttctatggtgtccaggtatgtagtgggtgggaattcttagc 1385

QY 61 gggctaagaattgcaactctctgagggcaccctgttactggtctatgttcgcaagaccc 120

Db 1386 gggcttcgaattgcccacactgaagctcccatcacaggttccatgtttgggaagaatc 1445

QY 121 tactttgagatctagtaagaagagcgcaataactgtttatgtgtggaataataatcc 180

Db 1446 tactttgtgacatgtcttccaaagagtgccaattactgttgcctctgcctctaaagaat 1505

QY 181 gttagtttgatcttcttctgaggttgccttaggagacatgtatgaactaaagaagcc 240

Db 1506 acagggactgctctctatcagaggtgagctaggtcaggtgtaatactactagagcc 1565

QY 241 acgtccatggacaa---acctccaagagggaagcattcgaccagggttaggcaaaacc 297

Db 1566 aatcctaagggcgaaggttgcctcaaggttaaacatagaccacagggttggaagatg 1625

QY 298 gtccactggagtcagagtttg-----tgaagtgaggaggtatgtctgttccctgc 351

Db 1626 gctccaggttctgcccactctgcacccctgaatggagtagcagtcgcatgaccagca 1685

QY 352 ggaagccgggtgcatcatcaataggagcctcgaactcatgtacacatgacatcgtc 411

Db 1686 agtgacacaggaattctgaatccagatggttaccctcaactacacatgaatattgca 1745

QY 412 tacaacacatcccagggtgaagatgcagttcttctgctgaaggtgcgttccat 462

Db 1746 tataaccacacagggtccgtatgcgttacccttttaagggttcagttta 1796

RESULT 14

AAZ44287  
 ID AAZ44287 standard; cDNA; 1843 BP.

XX AAZ44287;

XX 31-MAR-2000 (first entry)

XX Human brain PARP2 cDNA.

XX PARP; poly(ADP-ribose) polymerase; human; murine; detection; sepsis;  
 KW diagnosis; therapy; necrosis; apoptosis; neurodegenerative illness;  
 KW ischemic tissue damage; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 3..1715

FT /\*tag= a

FT /product= "PARP2"

XX WO9964572-A2.

XX 16-DEC-1999.

XX 04-JUN-1999; 99WO-EP03889.

XX 05-JUN-1998; 98DE-1025213.

XX 01-MAR-1999; 99DE-1008837.

XX (BADI ) BASF AG.

XX Kock M, Hoeger T, Kroeger B, Otterbach B, Lubisch W, Lemaire H;

XX

DR WPI: 2000-087218/07.  
DR P-PSDB; AAF51174.  
XX Novel genes and proteins, antibodies and binding partners useful in  
PT diagnosis and therapy of energy deficiency associated disease  
PT conditions -  
XX Claim 7a; Page 49-52; 96pp; German.  
XX This invention describes novel human and murine poly(ADP-ribose)  
CC polymerase (PARP) homologues, which are characterised by an amino acid  
CC sequence with a functional NAD<sup>+</sup>-binding site and no zinc finger  
CC sequence motif. of general formula CX<sub>2</sub>CX<sub>2</sub>MX<sub>2</sub>C (I). The nucleic acid  
CC sequences, PARP homologues and antibodies are useful for analytic  
CC detection of PARP homologues and for identifying PARP effectors or  
CC binding partners, as well as for determining their effectiveness.  
CC PARP-binding partners are useful for the diagnosis or therapy of a  
CC disease condition, which is the result of a PARP protein, especially an  
CC energy deficiency, which may comprise tissue damage from cell death  
CC following necrosis or apoptosis. The disease condition may be chosen  
CC from a neurodegenerative illness, or sepsis or ischemic tissue damage,  
CC in particular neurotoxic disturbances, etc. This sequence encodes the  
CC human PARP2 protein used in the method of the invention.  
XX  
XX Sequence 1843 BP; 599 A; 377 C; 447 G; 420 T; 0 other;  
Query Match 25.9%; Score 122.6; DB 21; Length 1843;  
Best Local Similarity 56.9%; Pred. No. 9e-31;  
Matches 268; Conservative 0; Mismatches 194; Indels 9; Gaps 2;  
Qy 1 acaagatgctattatgacaggttcaaggttgacgaattttgtgggaattcttagtcaa 60  
Db 1227 aacaggatgctctctatgctggttccagagtgatgtaactgggtgggaattctgagccat 1286  
Qy 61 gggctgaagaattgacacctctctgagccctgttactggttatgttgcggcaagggcctc 120  
Db 1287 gggctgaagaattgacacctctctgagccctgttactggttatgttgcggcaagggcctc 1346  
Qy 121 tacttgcagatctagtaagaagagcgcaatactgttattgttgataggaataatcct 180  
Db 1347 tacttgcagatctagtaagaagagcgcaatactgttattgttgataggaataatcct 1406  
Qy 181 gtaggttgatgctctctctgaggttgccttttagagacatgtatgaactaaagaagcc 240  
Db 1407 acaggaactgctctctatcagaagtgccttagtgcagtgtaactactagagggcc 1466  
Qy 241 acgtccatggacaa---acctccaagagggaagcattcgacccaaggattaggaacaaacc 297  
Db 1467 aatcctaaggccgaaggattgcttcaagggttaaacatagcaccagggtgggcaagatg 1526  
Qy 298 gtgccaactggagtcagaggtttg-----tgaagtggaggatgatgctgtagttccctgc 351  
Db 1527 gctccaggttctgcccactctgctcacccctgaatggggatgacagtgccattaggaacagca 1586  
Qy 352 ggaagcgggtgccaatcatcatttaggagctctgaactcattgatacaatgatactgcgc 411  
Db 1587 agtgacacagaattctgaatccagatggtttataccctcaactcaatgaatatatgta 1646  
Qy 412 tacaacacatcccggtggaagatgcaggtcttctgtggaagggtggtttccat 462  
Db 1647 tataaccccaaccagggtcgtgctgacgttacccttttaaaagggttcagtttaat 1697

RESULT 15  
AAC82090  
ID AAC82090 standard; cDNA; 1843 BP.  
XX  
XX AAC82090;  
XX  
DT 02-MAR-2001 (first entry)  
XX  
DE Human brain poly-ADP-ribose-polymerase cDNA.

XX Human; poly ADP-ribose polymerase; PARP; neuroprotective; nootropic;  
KW cerebroprotective; antiparkinsonian; nephrotropic; cardiatic; vasotropic;  
KW anticonvulsant; cytostatic; antibacterial; immunosuppressive; treatment;  
KW antinflammatory; antirheumatic; antiarthritic; antidiabetic; epilepsy;  
KW 2H-phthalazin-1-one derivative; neurodegenerative disease; tumor;  
KW neuronal damage; Alzheimer's disease; Huntington's disease; metastasis;  
KW Parkinson's disease; ischemic damage; microinfarction; sepsis;  
XX diabetes mellitus; ss.  
XX Homo sapiens.  
XX DE19921567-A1.  
XX 16-NOV-2000.  
XX 11-MAY-1999; 99DE-1021567.  
XX 11-MAY-1999; 99DE-1021567.  
XX (BADI ) BASF AG.  
XX Lubisch W, Sadowski J, Kock M, Hoeger T;  
DR WPI: 2001-032983/05.  
DR P-PSDB; AAB11480.  
XX  
XX Drugs for inhibiting PARP or especially homologous enzymes comprising  
PT 4-substituted phthalazinone derivatives, useful e.g. for treating  
PT neurodegenerative disease, ischemic damage, tumors or diabetes -  
XX  
XX Example A; Page 9-12; 14pp; German.  
XX This invention describes novel 4-substituted 2H-phthalazin-1-one  
CC derivatives (I) which are used for the treatment or prophylaxis of  
CC diseases associated with elevated poly-(ADP-ribose)-polymerase (PARP;  
CC EC 2.4.2.30) activity. The products of the invention have nootropic,  
CC neuroprotective, cerebroprotective, antiparkinsonian, nephrotropic,  
CC cardiatic, vasotropic, anticonvulsant, cytostatic, antibacterial,  
CC immunosuppressive, antinflammatory, antirheumatic, antiarthritic,  
CC antidiabetic. (I) are especially used for treating or preventing  
CC neurodegenerative disease or neuronal damage (especially associated  
CC with ischemia, trauma or massive bleeding, especially apoplexy or  
CC spinal-cranial trauma; or Alzheimer's disease, Huntington's disease or  
CC Parkinson's disease), treating or preventing ischemic damage  
CC (specifically renal damage after renal ischemia or during and after  
CC kidney transplantation or heart damage after cardiac ischemia), treating  
CC epilepsy, specifically generalized epileptic attacks (e.g. temporal lobe  
CC tonic-clonic attacks) or partial epileptic attacks (e.g. temporal lobe  
CC and complex partial attacks), treating microinfarction (e.g. during and  
CC after heart valve replacement, aneurysm resectioning and heart  
CC transplantation), revascularization of critically constricted coronary  
CC arteries (e.g. after PCTA or by-pass operations) or peripheral arteries  
CC (e.g. leg arteries), treating acute myocardial ischemia and damage during  
CC or after its mechanical or drug-induced lysis and treating tumors and  
CC their metastasis, sepsis and septic shock, inflammatory and rheumatic  
CC disease (e.g. rheumatoid arthritis), and diabetes mellitus. Although (I)  
CC inhibit PARP (i.e. the known form designated PARP1), they especially  
CC selectively and strongly inhibit PARP homologs, specifically the homolog  
CC PARP2. In particular (I) have very strong PARP2 inhibitory activity (e.g.  
CC with K<sub>i</sub> values of 1-20 nM) and high selectivity for PARP2 relative to  
CC PARP1 (generally by a factor of more than 5).  
XX  
XX Sequence 1843 BP; 599 A; 377 C; 447 G; 420 T; 0 other;  
Qy  
Db

QY 61 gggctagaagtgcacctctgaggcacctgttactggcttatatgttcggcaaggcctc 120  
Db 1287 gggcttcgaattgccccacctgaagctccatcacaggttacatgtttgggaaggaaac 1346  
QY 121 taatttgcagatctagtaagcaagagcgacacatactgtttatgtggatagggaataatcct 180  
Db 1347 taatttgcagatctgcttcccaagagtgccaatctactgtttgcctctgcctaaagaat 1406  
QY 181 gtagggttgatgcttcttctgaggttgcctttagagacatgtatgaactaaagaagccc 240  
Db 1407 acaggactgctctcttaacagaggtagctcttaggtcagtgtaatgaactactagagcc 1466  
QY 241 acgtccatggacaa----acctccaagagggaagcattcgacccaaggattaggcaaaacc 297  
Db 1467 aatcctaaggccgaaggattgcttcaaggtaaacatagcaccacaaaggctggcgaagatg 1526  
QY 298 gtgccaactggagtcagagtttg-----tgaagtgaggaggtgatgtcgtagttccctgc 351  
Db 1527 gctcccaagttctgcccactctgacccctgaatggaggtacagtgccattaggaccagca 1586  
QY 352 ggcgaagccggtgccatcatcaattaggagctctgaactcactgtacaatgagtacatcgtc 411  
Db 1587 agtgacacaggaattctgaatccagatggttataccctcaactacaatgaatatattgta 1646  
QY 412 tacaacacatcccaggtgaagatgcagttcttctgctgaagggtgcgtttccat 462  
Db 1647 tataaccaccaaccagggtccgtatgcgtacaccttttaaaaggttcagtttaaat 1697

Search completed: March 7, 2002, 18:16:38  
Job time: 13288 sec

Sequence 2, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 22, Appli  
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Sequence 22, Appli  
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Sequence 58, Appli  
Sequence 65, Appli  
Sequence 65, Appli  
Sequence 62, Appli  
Sequence 62, Appli  
Sequence 63, Appli  
Sequence 63, Appli  
Sequence 10, Appli  
Sequence 64, Appli  
Sequence 64, Appli

US-08-651-472-2  
US-08-651-472-3  
US-08-358-928-2  
US-08-358-928-3  
US-07-750-080A-22  
US-08-651-472-22  
US-08-358-928-22  
US-09-232-200-58  
US-09-232-197-58  
US-08-651-472-65  
US-08-358-928-65  
US-08-651-472-62  
US-08-358-928-62  
US-08-651-472-63  
US-08-358-928-63  
US-08-232-463-10  
US-08-651-472-64  
US-08-358-928-64

ALIGNMENTS

RESULT 1  
US-08-044-618-5  
; Sequence 5, Application US/08044618  
; Patent No. 5449605  
; GENERAL INFORMATION:  
; APPLICANT: SMULSON, MARK  
; TITLE OF INVENTION: METHOD OR DETECTING A PREDISPOSITION TO  
; TITLE OF INVENTION: CANCER BY THE USED OF RESTRICTION FRAGMENT LENGTH  
; TITLE OF INVENTION: POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE)  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1225 Connecticut Suite 300  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/044,618  
; FILING DATE: 19930406  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/257,696  
; FILING DATE: 14-OCT-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOX, SAMUEL L  
; REGISTRATION NUMBER: 30,353  
; REFERENCE/DOCKET NUMBER: 0654.0490001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)466-0800  
; TELEFAX: (202)833-8716  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3747 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-044-618-5

Query Match 29.4% Score 139.4; DB 1; Length 3747;  
Best Local Similarity 57.6%; Pred. No. 2.6e-37;  
Matches 270; Conservative 0; Mismatches 196; Indels 3; Gaps 1;

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model  
Run on: March 7, 2002, 16:49:07 ; Search time 122.78 Seconds  
(without alignments)  
874.333 Million cell updates/sec

Title: US-09-236-995D-3  
Perfect score: 474  
Sequence: 1 aacaagatgctattatgca.....gtttccatcacaaagagtag 474

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues 702406  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	139.4	29.4	3747	1 US-08-044-618-5	Sequence 5, Appli
2	137.8	29.1	5345	1 US-08-044-618-7	Sequence 7, Appli
3	136.2	28.7	2682	1 US-08-044-618-3	Sequence 3, Appli
4	114.6	24.2	595	4 US-09-328-111-216	Sequence 216, App
5	108.8	23.0	1592	1 US-08-044-618-4	Sequence 4, Appli
6	31	6.5	7218	1 US-08-232-463-14	Sequence 14, Appli
7	30.6	6.5	2757	2 US-08-627-254C-26	Sequence 26, Appli
8	30.4	6.4	2625	2 US-08-357-533A-1	Sequence 1, Appli
9	30.4	6.4	2625	2 US-08-459-009-1	Sequence 1, Appli
10	30.4	6.4	2625	3 US-08-459-951-1	Sequence 1, Appli
11	29.8	6.3	1160	1 US-07-780-973-15	Sequence 15, Appli
12	29.4	6.2	3580	4 US-09-081-345-1	Sequence 1, Appli
13	28.4	6.0	1743	2 US-08-841-178-20	Sequence 20, Appli
14	28.4	6.0	2947	1 US-08-457-176-1	Sequence 1, Appli
15	28.4	6.0	2976	1 US-08-457-175-1	Sequence 1, Appli
16	28.4	6.0	2976	4 US-09-352-168-26	Sequence 26, Appli
17	28.4	6.0	2976	4 US-09-352-168-26	Sequence 26, App
18	27.6	5.8	328	4 US-09-385-982-227	Sequence 227, App
19	27.6	5.8	758	4 US-09-328-111-685	Sequence 685, App
20	27.2	5.7	3236	4 US-08-927-219-7	Sequence 7, Appli
21	27.2	5.7	3238	4 US-08-927-219-1	Sequence 1, Appli
22	27.2	5.7	3238	4 US-08-927-219-3	Sequence 3, Appli
23	27.2	5.7	3239	4 US-08-927-219-5	Sequence 5, Appli
24	27.2	5.7	6254	4 US-08-927-219-126	Sequence 126, App
25	27	5.7	323	6 5252465-10	Patent No. 5252465
26	27	5.7	1133	1 US-07-750-080A-2	Sequence 2, Appli
27	27	5.7	1133	1 US-07-750-080A-3	Sequence 3, Appli



QY 1 aacaagatgctattatgacagcgttcaaggttgacgaattttgtgggaattcttagtcaa 60  
Db 2756 AACCGAAGATTGCTGTGGCAGCGGTCCAGGACCACTTGTCTGGGATCTCTGCCAG 2815  
QY 61 gggtctaaagattgacacctctgagcgcctgttactgtgcttatgttcggcaaggcctc 120  
Db 2816 GGTCTTCGATAGCCCGCTGGAAGCCGCTGACAGCGCTACATGTTGGTAAAGGATC 2875  
QY 121 tactttgcagatctagtaagcaagagcgacataactgttattgtgtaggaataatcct 180  
Db 2876 TATTTGCTGACATGGTCTCCAGAGTGCCCACTACTTACCATACGCTCTCAGGAGACCCA 2935  
QY 181 gtaggttgatgctcttctgtgaggttctttaggagacatgtatgaactaaagaagcc 240  
Db 2936 ATAGGCTTAATCTGTTGGGAGAAGTGGCCCTTGGAAACATGATGAACAGACGCT 2995  
QY 241 acgtccatgacaaacctcaagaggaagcattcgacaaaggattagggcaaacccgtg 300  
Db 2996 TCACATATCAGCAGGTACCAAGGCAAGCACAGTGTCAAAGGTTTGGGCAAACTACC 3055  
QY 301 ccactggagtcagagttgtggaagtggagggatgctgtagtccctgcgcaagccg 360  
Db 3056 CCTGATCTTCAG--CTAACATTAGTCTGGATGCTGACGTTCTCTTGGACCGGG 3112  
QY 361 gtccatcatcaattgagggctctgaactcatgtacatgtagtacctctacacaca 420  
Db 3113 ATTTCATCTGGTGTGAATGACACCTCTCTACTATATATAACGAGTACATGCTATGATATT 3172  
QY 421 tccaggtgaagatgcagttcttctgctgaaggtgcgtttccatcacacaaga 469  
Db 3173 GCTCAGGTAATCTGAAGTATCTGCTGAAGACTGAAATTCATTTTAAAGA 3221

## RESULT 2

US-08-044-618-7  
; Sequence 7, Application US/08044618  
; Patent No. 5449605  
; GENERAL INFORMATION:  
; APPLICANT: SMULSON, MARK  
; TITLE OF INVENTION: METHOD OR DETECTING A PREDISPOSITION TO  
; TITLE OF INVENTION: CANCER BY THE USED OF RESTRICTION FRAGMENT LENGTH  
; TITLE OF INVENTION: POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE)  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1225 Connecticut Suite 300  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/044,618  
; FILING DATE: 19930406  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/257,696  
; FILING DATE: 14-OCT-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOX, SAMUEL L  
; REGISTRATION NUMBER: 30,353  
; REFERENCE/DOCKET NUMBER: 0654.0490001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)466-0800  
; TELEFAX: (202)833-8716  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5345 base pairs  
; TYPE: NUCLEIC ACID

; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-044-618-7

## Query Match

Best Local Similarity 29.1%; Score 137.8; DB 1; Length 5345;  
Matches 269; Conservative 0; Mismatches 197; Indels 3; Gaps 1;

QY 1 aacaagatgctattatgacagcgttcaaggttgacgaattttgtgggaattcttagtcaa 60  
Db 3519 AACTGAAGGTGCTGTGGCATGGGTCCAGGACCACTTGTCTGGGATCTCTGCCCTG 3578  
QY 61 gggtctaaagattgacacctctgagcgcctgttactgtgcttatgttcggcaaggcctc 120  
Db 3579 GGTCTTTGGATAGCCCTGCCGTAAGCAGCTGTGATGGGCTACATGTTGGTAAAGTATC 3638  
QY 121 tactttgcagatctagtaagcaagagcgacataactgttattgtgtaggaataatcct 180  
Db 3639 TATTTGCTGATGCTTGTCTCAAGAGTGCACAGCTGCCATACATCTTAGGAAGACCCA 3698  
QY 181 gtaggtttgagctcttctgtgaggttctttaggagacatgtatgaactaaagaagcc 240  
Db 3699 ATAGGTTAATCTCTCGAAGAAAGTTGCCCTTGGAAACGTTGTGTAACGATGCT 3758  
QY 241 acgtccatgacaaacctcccaagaggaagcattcgacaaaggattagggcaaacccgtg 300  
Db 3759 TCACATATCAGCAAGTTACCAAGGCAAGCACAGTGTCAAAGGTTTGGGCAAACTACT 3818  
QY 301 ccactggagtcagagttgtggaagtggagggatgctgtagtccctgcgcaagccg 360  
Db 3819 CCTGACCTTTCAG--CTAGTATCCCACTGGATGCTGAGGTTCTCTTGGGACCAAG 3875  
QY 361 gtccatcatcaattgagggctctgaactcatgtacatgtagtacctctacacaca 420  
Db 3876 GTTTCATCTGGTGTGAATGACACCTGCTACTGTATATAGTACATGTTCTGTATGATATT 3935  
QY 421 tccaggtgaagatgcagttcttctgctgaaggtgcgtttccatcacacaaga 469  
Db 3936 GCTCAGGTAATCTGAAGTATCTGCTGAAGACTGAAATTCATTTTAAAGA 3984

## RESULT 3

US-08-044-618-3  
; Sequence 3, Application US/08044618  
; Patent No. 5449605  
; GENERAL INFORMATION:  
; APPLICANT: SMULSON, MARK  
; TITLE OF INVENTION: METHOD OR DETECTING A PREDISPOSITION TO  
; TITLE OF INVENTION: CANCER BY THE USED OF RESTRICTION FRAGMENT LENGTH  
; TITLE OF INVENTION: POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE)  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1225 Connecticut Suite 300  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/044,618  
; FILING DATE: 19930406  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/257,696  
; FILING DATE: 14-OCT-1988  
; ATTORNEY/AGENT INFORMATION:

NAME: FOX, SAMUEL L  
REGISTRATION NUMBER: 30,353  
REFERENCE/DOCKET NUMBER: 0554.0490001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)466-0800  
TELEFAX: (202)833-8716  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2682 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-044-618-3

CURRENT APPLICATION NUMBER: US/09/328,111  
CURRENT FILING DATE: 1999-06-08  
EARLIER APPLICATION NUMBER: US 60/088,801  
EARLIER FILING DATE: 1998-06-10  
NUMBER OF SEQ ID NOS: 850  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 216  
LENGTH: 595  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(595)  
OTHER INFORMATION: n = A,T,C or G  
US-09-328-111-216

Query Match 24.2% Score 114.6; DB 4; Length 595;  
Best Local Similarity 63.3%; Pred. No. 2.6e-29;  
Matches 193; Conservative 0; Mismatches 109; Indels 3; Gaps 1;  
Qy 1 aacaagatgctattatggcagcgttcaaggttgacgaattttgtgggaattcttagtcaa 60  
Db 342 AACAGGATGCTTCTATGGCATGGTTCAGGATGAGTAACTGCTGGGAAATCTTGAGCCAT 283  
Qy 61 gggctaaagaattgcacctctgagcaccctgttactggctatatgttggcgaaggcctc 120  
Db 282 GGGCTTCGAATGCCCCACCTGAAGCTCCCATCAGGTTACATGTTTGGGAAAGGAATC 223  
Qy 121 tactttgagatctagttaagaagaagcacaataacttctttagtggaatgaataatc 180  
Db 222 TACTTTGCTGACATCTTCCAGAGTGCCTAACTACTGCTTTCCTCTCGCTAAAGAAAT 163  
Qy 181 gtagggttgatgctctcttctgaggttctttaggagacatgtatgaactaaagaagcc 240  
Db 162 ACAGGACTGCTGCTCTTATCAGAGGTAGCTCTAGGTCACTGTAATGAATAGAGGCC 103  
Qy 241 acgtccatggacaa---acgtccaaagaggaagcattcgacaaaggttaggcaaaacc 297  
Db 102 AATCCTAAGGCCGAAGGATTTGCTTCAAGGTAACATAGCACCAAGGGCTGGGCAAGATG 43  
Qy 298 gtgcc 302  
Db 42 GCTCC 38

Query Match 28.7% Score 136.2; DB 1; Length 2682;  
Best Local Similarity 57.1%; Pred. No. 2.7e-36;  
Matches 268; Conservative 0; Mismatches 198; Indels 3; Gaps 1;  
Qy 1 aacaagatgctattatggcagcgttcaaggttgacgaattttgtgggaattcttagtcaa 60  
Db 2050 AACTGAAGGTGCTGTGGATGGTCTCAGGACCAACCAACTTCTGGGATCCTGTCCCTG 2109  
Qy 61 gggctaaagaattgcacctctgagcaccctgttactggctatatgttgcgaaggcctc 120  
Db 2110 GGTCTTTGGATACCCCTGCTGAAGCACCTGTGATGGCTACATGTTTGGTAAAGTGATC 2169  
Qy 121 tactttgagatctagttaagaagaagcacaataacttctttagtggaatgaataatc 180  
Db 2170 TATTTCGCTGATCTGTCTCAAGAGTGCCACGACTGCCATACATCTTAGGAAGACCCA 2229  
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Db 2230 ATAGGGTTAATCTGCGGAAGAGTGGCCCTTGGAAACGTGTGTAACCTGAAGCAATGCT 2289  
Qy 241 acgtccatggacaaacctccaaaggaagcattcgacaaaggttaggcaaaaccgtg 300  
Db 2290 TCACATATCAGCAGATTTACCCAAAGGCAAGCAGATGTCAAAGGTTTGGGCAAACTACT 2349  
Qy 301 ccactggagtcagattgttgaggtgagggatgctgtagtccctcgcggcaagccg 360  
Db 2350 CCTGACCTTTTCTAGTATCCACTGGATGGTGTAGAGGTTCCTCTTGGGACCCAGG 2406  
Qy 361 gtgccatcatcaatgaagcctcgaactcatgtacatgaatgacatgctctacacaca 420  
Db 2407 GTTTTCATCTGTGTGAATGACACTGCTCTACTGTTTAAATGAGTACATGCTATGATATT 2466  
Qy 421 tccaggtgaagatgcagttcttctgctgaaggtgcgttcccatcacaaga 469  
Db 2467 GCTCAGGTAATCTGAAATATCTCTGTAAGTGAATTTCAATTTTAAAGA 2515

RESULT 5  
US-08-044-618-4  
Sequence 4, Application US/08044618  
Patent No. 5449605  
GENERAL INFORMATION:  
APPLICANT: SMULSON, MARK  
TITLE OF INVENTION: METHOD OR DETECTING A PREDISPOSITION TO  
TITLE OF INVENTION: CANCER BY THE USED OF RESTRICTION FRAGMENT LENGTH  
TITLE OF INVENTION: POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE)  
TITLE OF INVENTION: POLYMERASE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESS: Sterne, Kessler, Goldstein & Fox  
STREET: 1225 Connecticut Suite 300  
CITY: Washington  
STATE: D.C.  
ZIP: 20036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/044,618  
FILING DATE: 19930406  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

Query Match 28.7% Score 136.2; DB 1; Length 2682;  
Best Local Similarity 57.1%; Pred. No. 2.7e-36;  
Matches 268; Conservative 0; Mismatches 198; Indels 3; Gaps 1;  
Qy 1 aacaagatgctattatggcagcgttcaaggttgacgaattttgtgggaattcttagtcaa 60  
Db 2050 AACTGAAGGTGCTGTGGATGGTCTCAGGACCAACCAACTTCTGGGATCCTGTCCCTG 2109  
Qy 61 gggctaaagaattgcacctctgagcaccctgttactggctatatgttgcgaaggcctc 120  
Db 2110 GGTCTTTGGATACCCCTGCTGAAGCACCTGTGATGGCTACATGTTTGGTAAAGTGATC 2169  
Qy 121 tactttgagatctagttaagaagaagcacaataacttctttagtggaatgaataatc 180  
Db 2170 TATTTCGCTGATCTGTCTCAAGAGTGCCACGACTGCCATACATCTTAGGAAGACCCA 2229  
Qy 181 gtagggttgatgctctcttctgaggttctttaggagacatgtatgaactaaagaagcc 240  
Db 2230 ATAGGGTTAATCTGCGGAAGAGTGGCCCTTGGAAACGTGTGTAACCTGAAGCAATGCT 2289  
Qy 241 acgtccatggacaaacctccaaaggaagcattcgacaaaggttaggcaaaaccgtg 300  
Db 2290 TCACATATCAGCAGATTTACCCAAAGGCAAGCAGATGTCAAAGGTTTGGGCAAACTACT 2349  
Qy 301 ccactggagtcagattgttgaggtgagggatgctgtagtccctcgcggcaagccg 360  
Db 2350 CCTGACCTTTTCTAGTATCCACTGGATGGTGTAGAGGTTCCTCTTGGGACCCAGG 2406  
Qy 361 gtgccatcatcaatgaagcctcgaactcatgtacatgaatgacatgctctacacaca 420  
Db 2407 GTTTTCATCTGTGTGAATGACACTGCTCTACTGTTTAAATGAGTACATGCTATGATATT 2466  
Qy 421 tccaggtgaagatgcagttcttctgctgaaggtgcgttcccatcacaaga 469  
Db 2467 GCTCAGGTAATCTGAAATATCTCTGTAAGTGAATTTCAATTTTAAAGA 2515

RESULT 4  
US-09-328-111-216/c  
Sequence 216, Application US/09328111  
Patent No. 6262333  
GENERAL INFORMATION:  
APPLICANT: Endege, Wilson O.  
APPLICANT: Steinmann, Kathleen E.  
APPLICANT: Astle, Jon H.  
APPLICANT: Burgess, Christopher C.  
APPLICANT: Bushnell, Steven E.  
APPLICANT: Carroll III, Eddie  
APPLICANT: Catino, Theodore J.  
APPLICANT: Derti, Adnan  
APPLICANT: Ford, Donna M.  
APPLICANT: Lewis, Marcia E.  
APPLICANT: Monahan, John E.  
APPLICANT: Schlegel, Robert  
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
TITLE OF INVENTION: PRODUCTS  
FILE REFERENCE: CCD-257 (US)

APPLICATION NUMBER: US/07/257,696  
FILING DATE: 14-OCT-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: FOX, SAMUEL L  
REGISTRATION NUMBER: 30,353  
REFERENCE/DOCKET NUMBER: 0654.0490001  
TELEPHONE: (202)466-0800  
TELEFAX: (202)833-8716  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1592 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-044-618-4

Query Match 23.0%; Score 108.8; DB 1; Length 1592;  
Best Local Similarity 60.5%; Pred. No. 3.9e-27;  
Matches 179; Conservative 0; Mismatches 117; Indels 0; Gaps 0;  
QY 1 aacaagactattatggcaggttcaaggttgacgaattttgtgggaatttttagtcaa 60  
Db 1209 AACTGAAGGTGCTGTGGCATGGTCCAGGACCACCAACTTTGCTGGGATCCTGTCCTG 1268  
QY 61 gggcgaagattgacacctctgagcagcctgttactggctatatgttcgcaaaagccctc 120  
Db 1269 GGTCTTTGGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1328  
QY 121 tacttgcagatctagtgaagcagcagcagcagcagcagcagcagcagcagcagcagc 180  
Db 1329 TATTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1388  
QY 181 gtagggttgccttcttcttgcaggttctttagagacatgtatgaactaaagaaagcc 240  
Db 1389 ATAGGGTTAATCTGTCGGAGAAAGTGGCCCTTGGAACAGGTGTGTGAACGAACATGCT 1448  
QY 241 acgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 296  
Db 1449 TCACATATCAGCAAGTTACCCCAAGGCAAGCACAGTGTCAAGAGTTTGGGGCAAAAC 1504

RESULT 6  
US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEFFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-Fls  
US-08-232-463-14

Query Match 6.5%; Score 31; DB 1; Length 7218;  
Best Local Similarity 6.1%; Pred. No. 2;  
Matches 25; Conservative 198; Mismatches 188; Indels 0; Gaps 0;  
QY 28 aggttgacgaattttgtgggaatttttagtcaaggcgttaagaaattgcacacctcctgagcga 87  
Db 1453 AGATAGAAGATTTGGTACRR 1394  
QY 88 cctgtactggctatgttcgcgcaagcctctactttgcagatctagtaagcaagc 147  
Db 1393 RRR 1334  
QY 148 gcaacatctgttctgtgtaggaataatcctgtgaggtttgtgaggtttcttctgaggtt 207  
Db 1333 RRR 1274  
QY 208 gctttgagcagatgtatgaactaaagaaagccacgtccatggacaaacctcgaagagg 267  
Db 1273 RRR 1214  
QY 268 agcattcgcacgaaggattaggcaaacccgtgccactggagtcagagttgtgaaagtg 327  
Db 1213 RRR 1154  
QY 328 agggatgtgtgttctcctgcgcgcaagcoggtgcccatacctaattagagctctgaa 387  
Db 1153 RRR 1094  
QY 388 ctcatgtacaatgagtcacatcgtctacaacacatcccagggtgaagatgcag 438  
Db 1093 RRR 1043

RESULT 7  
US-08-627-254C-26/c  
Sequence 26, Application US/08627254C  
Patent No. 5859229  
GENERAL INFORMATION:  
APPLICANT: Kniss, Douglas A.  
TITLE OF INVENTION: Elcosanoid Formation  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Calfee, Halter & Grilwold LLP  
STREET: 800 Superior Avenue  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: USA  
ZIP: 44114  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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RESULT      8
US-08-357-533A-1/c
; Sequence 1, Application US/08357533A
; Patent No. 5831050
; GENERAL INFORMATION:
; APPLICANT: JIN, DONALD F
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: SMART, JOHN E
; TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
; ADDRESSEE: INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,533A
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-073FW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)-435-9001
; TELEFAX: (508)-435-0992
; INFORMATION FOR SEQ ID NO: 1:

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RESULT          9
US-08-459-009-1/c
; Sequence 1, Application US/08459009
; Patent No. 5861479
; GENERAL INFORMATION:
; APPLICANT: JIN, DONALD F
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: SMART, JOHN E
; TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
; ADDRESSEE: INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,009
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,533
; FILING DATE: 16-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP-073FW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)-435-9001
; TELEFAX: (508)-435-0992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2625 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:

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QY 188 tgaTg 192  
Db 945 TGATG 949

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; EARLIER APPLICATION NUMBER: US 08/433,111
; EARLIER FILING DATE: 1995-05-03
; EARLIER APPLICATION NUMBER: US 07/959,506
; EARLIER FILING DATE: 1992-10-09
; EARLIER APPLICATION NUMBER: US 07/476,661
; EARLIER FILING DATE: 1990-02-12
; EARLIER APPLICATION NUMBER: US 07/315,355
; EARLIER FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 20
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: structural gene encoding B.t.k. HD-1 insectidal
; OTHER INFORMATION: protein
; US-08-841-178-20

Query Match          6.0%; Score 28.4; DB 2; Length 1743;
Best Local Similarity 56.4%; Pred. No. 7.5; Mismatches 41; Indels 0; Gaps
Matches 53; Conservative

QY 306 ggaagtcagagttgtgaaagtgaggatgatgtcgtatgtccctcgcgcaagcogtgc 365
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Db 1345 GGATTGGGTGATTGTTGATGAAGGATGATCTTTTGAACACTCAGCAGTGTATCC 1386
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QY 366 atcatcaattagagctctgaactcatgtacaat 399
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Db 1285 AAGACAGACATAGGAGCTCTTATTACTTACAT 1252
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RESULT 14
US-08-457-176-1/c
; Sequence 1, Application US/08457176
; Patent No. 5591826
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: de la Chappelle, Albert
; TITLE OF INVENTION: Mutator Gene and Hereditary
; TITLE OF INVENTION: No. 5591826-Polyposis Colorectal Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie, and Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,176
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160295
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.44900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:

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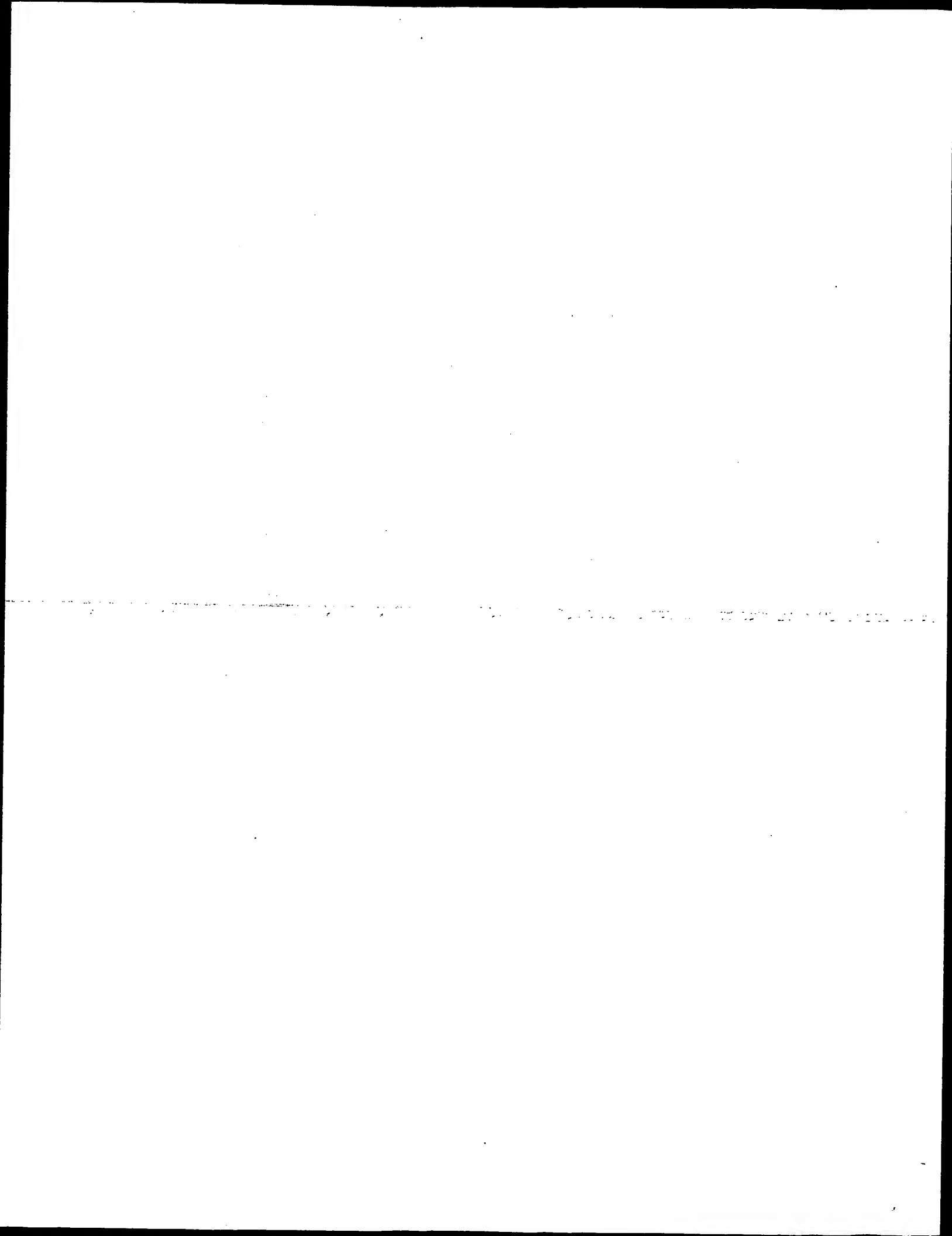
RESULT 15
US-08-457-175-1/c
; Sequence 1, Application US/08457175
; Patent No. 5693470
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: de la Chappelle, Albert
; TITLE OF INVENTION: Mutator Gene and Hereditary
; TITLE OF INVENTION: No. 5693470-Polyposis Colorectal Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie, and Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,175
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160295
; FILING DATE: 02-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.44900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202.508.9100
; TELEFAX: 202.508.9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2947 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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Search completed: March 7, 2002, 16:49:28  
Job time: 8158 sec







GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2002, 15:24:26 ; Search time 2934.5 Seconds  
(without alignments)  
1735.730 Million cell updates/sec

Title: US-09-236-995D-3

Perfect score: 474

Sequence: 1 aacaagatgctattatggca.....gtttccatcacaaaggtag 474

Scoring table:

IDENTITY\_NUC

Gap 10.0, Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estfun:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estom:\*  
5: em\_estpl:\*  
6: em\_estba:\*  
7: em\_estro:\*  
8: em\_estov:\*  
9: em\_hic:\*  
10: gb\_est1:\*  
11: gb\_est2:\*  
12: gb\_hic:\*  
13: gb\_gss:\*  
14: em\_gss\_fun:\*  
15: em\_gss\_hum:\*  
16: em\_gss\_inv:\*  
17: em\_gss\_pln:\*  
18: em\_gss\_pro:\*  
19: em\_gss\_rod:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	312	65.8	536	10	BE419432
3	299	63.1	661	10	AV834168
4	269.2	56.8	369	10	BE420229
5	189	39.9	502	11	BE420229
6	186.2	39.3	419	11	BE941860
7	161.4	34.1	661	10	AV833893
8	155.8	32.9	442	11	D42790
9	152.2	32.1	716	11	BE1217470
10	150.6	31.8	587	11	BE911127
11	150.6	31.8	725	11	BE1079902
12	142.6	30.1	571	10	BE304535

13	142.6	30.1	579	10	AA397988
14	142.6	30.1	669	10	AA401836
15	142.6	30.1	916	11	BI093436
16	142.6	30.1	952	11	BF793705
17	142.6	30.0	678	11	BF101770
18	141	29.7	709	10	BE382739
19	140.8	29.7	928	11	BE675913
20	136.8	28.9	487	10	AW144795
21	134.6	28.4	563	10	AA263755
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23	133.6	28.2	861	11	BE280821
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25	130	27.4	688	10	BE729084
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27	127.4	26.9	990	11	BG031594
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29	124.6	26.3	763	11	BF393399
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36	122.2	25.8	634	11	BI196670
37	121.6	25.7	499	10	BE488132
38	121	25.5	603	10	AI417842
39	120.4	25.4	617	10	AA212857
40	117.8	24.9	897	11	BE884815
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42	116.2	24.5	465	10	AA608364
43	115.6	24.4	445	10	AA270953
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45	114.8	24.2	438	10	BE334294

#### ALIGNMENTS

RESULT 1

BF255013

LOCUS 607 bp mRNA

DEFINITION HVSMEF0005L18f Hordeum vulgare seedling root EST library HVCDNA0007 (etiolated and unstressed) Hordeum vulgare cdna clone

ACCESSION HVSMEF0005L18f, mRNA sequence.

VERSION BF255013

KEYWORDS EST.

SOURCE BF255013.2 GI:13117445

ORGANISM barley.

Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

; Triticeae; Hordeum.

1 (bases 1 to 607)

Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu

, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo

, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and

Wood, T.

Development of a genetically and physically anchored EST resource

for barley genomics

Unpublished (2000)

On Nov 16, 2000 this sequence version replaced gi:11184130.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: AATTAACTCTACTAAAGG

High quality sequence stop: 551.

Location/Qualifiers

1..607

/organism="Hordeum vulgare"

/cultivar="Morex"  
 /db\_xref="taxon:4513"  
 /clone="HVSMBF0005L18f"  
 /clone\_lib="Hordeum vulgare seedling root EST library  
 HVCNDA0007 (etiolated and unstressed)"  
 /tissue\_type="Seedling root"  
 /lab\_host="TJ121"  
 /note="Vector: lambdaZAP; Site\_1: EcoRI; Site\_2: XhoI; For  
 more details on library preparation and sequence analysis  
 see http://www.genome.clemson.edu/projects/barley/ To  
 order a clone see http://www.genome.clemson.edu/orders"  
 BASE COUNT 165 a 113 c 163 g 166 t  
 ORIGIN

Query Match 71.4%; Score 338.2; DB 11; Length 607;  
 Best Local Similarity 85.6%; Pred. No. 1.4e-91;  
 Matches 376; Conservative 0; Mismatches 63; Indels 0; Gaps 0;  
 Oy 34 acgaatttgggaattcttagtcaagggtcgaagattgacacctctgagggcactgtt 93  
 Db 1 ACAATTTTATGGAAATCTTAGTCAGGACTAAGATAGCACCCTCTGAGGCCCGCTG 60  
 Oy 94 actggtatattgtcggaaggcctctactttgcagatctagtaagcagaagcgcaaa 153  
 Db 61 AGGGCTATATGTTGGCAAGGCTCTACTTTGCAGATTTAGTAAGCAAGGTGCACAG 120  
 Oy 154 tactgttatgtgtagaagaataacctgtgaggttgatgtcttctgaggttgcttta 213  
 Db 121 TATTGTTATGTGGATAGAAAAATCCGACTGGCTGTGATGCTCTTTCTGAGGTTGCTCTA 180  
 Oy 214 ggaacatgtatgaactaaagaaagccacgtccatgacaaacctcaagaggaagcat 273  
 Db 181 GGACATGATGATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 240  
 Oy 274 tcgaccaaggatttaggcaaacctgcccactgaggtcagagtttggagtgaggat 333  
 Db 241 TCGACCAAGGCTTATAGGCAAACTGTGCCACTAGAGTCGGAGTTTGTAAATGGAGGAT 300  
 Oy 334 gatctgtagtcttcctggcgaacccggtgccatcatcaattaggagctctgaactcatg 393  
 Db 301 GATGTCGTCGTCCTTGTGGCAAGCCAGTCCAGCAGTCTATCAGGGCATCTGAGCTTCG 360  
 Oy 394 tacaatgagtcacgtctcaacacacacacacacacacacacacacacacacacacac 453  
 Db 361 TACAACGAGTATATAGTGTACACACAGCTCAGGTGAAGATGACAGTCTCTTTGTTGAAGTTC 420  
 Oy 454 cgttccatcacagaggt 472  
 Db 421 AAATTCCTCACAAGCGTT 439

RESULT 2  
 BE419432 536 bp mRNA 24-JUL-2000  
 LOCUS WWS012.A12R000101 ITEC WMS Wheat: Scutellum Library Triticum  
 DEFINITION aestivum cDNA clone WWS012.A12, mRNA sequence.  
 BE419432  
 BE419432.1 GI:9417278  
 VERSION EST.  
 KEYWORDS bread wheat.  
 SOURCE Triticum aestivum  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
 : Triticeae; Triticum.  
 1 (bases 1 to 536)  
 REFERENCE  
 AUTHORS Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier,  
 S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P.,  
 Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P.,  
 Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,  
 Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,  
 Sorrells, M., Warburton, M., and Wenzel, G.  
 TITLE International Triticaceae EST Cooperative (ITEC): Production of

Expressed Sequence Tags for Species of the Triticeae  
 Unpublished (2000)  
 Contact: Schuch, W.  
 Zeneca Wheat Improvement Centre, Norwich Research Park  
 Colney Lane, Norwich NR4 7UH UNITED KINGDOM  
 Tel: 44 1603 250 2600  
 Fax: 44 1603 250 699  
 Email: wolfgang.schuch@zeneca.com  
 International Triticeae EST Cooperative (ITEC)  
 http://wheat.pw.usda.gov/genome.  
 Location/Qualifiers  
 1. 536  
 /organism="Triticum aestivum"  
 /cultivar="Novosibirskaya 67"  
 /db\_xref="taxon:4565"  
 /clone="WWS012.A12"  
 /clone\_lib="ITEC WMS Wheat Scutellum Library"  
 /tissue\_type="scutellum callus"  
 /note="M13 Reverse sequencing primer used for 5' end of  
 clone."

BASE COUNT 143 a 106 c 144 g 139 t 4 others  
 ORIGIN  
 Query Match 65.8%; Score 312; DB 10; Length 536;  
 Best Local Similarity 85.1%; Pred. No. 1.2e-83;  
 Matches 348; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
 Oy 64 ctaagaattgcacctctgagggcactgttactggtctatatgttcggcaaaagcctctac 123  
 Db 5 CGAGGGATAGCACCTCTCTGAGGCTCTCTGTGACAGGCTATATGTTGGCAAGGCTCTAC 64  
 Oy 124 ttgcagatctagtaagcagaagcacaactacttattgtgtagaataactctgta 183  
 Db 65 TTTCAGATTTAGTAGCAAGAGTGCACAGTATTGTTATGTGGATAGAAAAATCCGACT 124  
 Oy 184 ggttgcagctctcttctgaggttgccttttagagacatgtatgaactaaagaaagccag 243  
 Db 125 GCTTCATCTCTTCTTCTGAGGTTGCTCTAGGAGACATGCATGAACGAAAGGCCAGC 184  
 Oy 244 tcatggacaacctccaaagagggaagcaattcgacaagggattaggcaaaacccgtgca 303  
 Db 185 CCAATGGACAAACCTCCAAAGAGAAAGCAATTCGACCAAGGGCTTAGAAAAAATCTGCGG 244  
 Oy 304 ctggagtcaggtttgtgaagtggaggatgatgtcgttagtccctcgccaagccggtg 363  
 Db 245 CTAGAGTCGAGTGTGTGAATGGAGGATGATATCGTCGCTCTTGGCAAGCCAGTG 304  
 Oy 364 ccacatcaattagagctctgaactcatgtacaatgagacatcgtctacaacacatcc 423  
 Db 305 CCAGCATCTATCANGGCATCTCAGCTTCTGTACAACGAGTATATAGTCTACAACAGCC 364  
 Oy 424 cagggtgaagatcagttctgtgaggtgcgtttccatcaccaagaggt 472  
 Db 365 CAGGTGAAGATCAGTCTTCTTGTGAAGGTCAGATTCCCGTCACAGCGTT 413

RESULT 3  
 AV834168/c 661 bp mRNA 22-JUN-2001  
 LOCUS AV834168 K. Sato unpublished cDNA library: Hordeum vulgare subsp.  
 DEFINITION vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA  
 clone rbags5k04, mRNA sequence.  
 AV834168  
 AV834168.1 GI:14526257  
 VERSION EST.  
 KEYWORDS Hordeum vulgare subsp. vulgare.  
 SOURCE Hordeum vulgare subsp. vulgare.  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
 : Triticeae; Hordeum.  
 1 (bases 1 to 661)  
 REFERENCE  
 AUTHORS Sato, K.

TITLE Barley EST sequencing project in NIG and Okayama Univ  
JOURNAL Unpublished (2001)  
COMMENT Contact: Kazuhiro Sato  
Research Institute for Bioresources  
Okayama University, Barley Germplasm Center  
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan  
Email: kzsato@rib.okayama-u.ac.jp,  
URL: http://www.rib.okayama-u.ac.jp/barley/  
Sato, K., Saisbo, D., Takeda, K., Shini, T. and Kohara, Y. Direct  
submission;  
database: http://www.shigen.nig.ac.jp/barley/Barley.html.

FEATURES source  
Location/Qualifiers  
1. .661  
/organism="Hordeum vulgare subsp. vulgare"  
/cultivar="Haruna Nijo"  
/db\_xref="taxon:112509"  
/clone="rbags5k04"  
/clone\_lib="K. Sato unpublished cDNA library: Hordeum  
vulgare subsp. vulgare shoots germination"  
/tissue\_type="shoots"  
/dev\_stage="germination"  
BASE COUNT 180 a 181 c 132 g 168 t  
ORIGIN

Query Match 63.1%; Score 299; DB 10; Length 661;  
Best Local Similarity 85.0%; Pred. No. 1.1e-79;  
Matches 346; Conservative 0; Mismatches 60; Indels 1; Gaps 1;  
QY 67 agaatgcaacctctgaggaacctgttta-ctggctatatatttcggcaaaagccctactt 125  
Db 661 AGGATAGCACTCTGTAGGCAACCCGTCACCGGCTATATGTTGGCAAGGCTCTACTT 602  
QY 126 tgcagatctagtaagcaagcgccacaactactgttatgtgataggaataatcctgtagg 185  
Db 601 TGCAGATTTAGTAAAGAGTGCACAGTATTGTTATGTGATAGAAAAATCCGACTGG 542  
QY 186 ttgatgtcttcttctgaggtgcttcttaggagacatgtatgaactaaagaagccacgtc 245  
Db 541 CTTGATGCTTCTTCTGAGGTGCTCTAGGAGACATTCATGAACCTGAAAAAGCAAGCC 482  
QY 246 catgacaaacctccaagaggaagcattcgaccagggattaggcaaaacccgtgccact 305  
Db 481 AATGGCAAAACCTCCAAAGAGGAAGCATTCGACCAAGGGCTTAGGCAAACTGTGCCACT 422  
QY 306 ggaatcagagtttgaagtgaggatgatgctgtagttccctgcgcaagccggtgcc 365  
Db 421 AGAGTCGAGCTTTGTTAAATGGAGGATGATGTCGTCGCTTGTGGCAAGCCAGTGC 362  
QY 366 atcatcaattaggagctctgaactcatgtacaaatgagtaacatcgtctacacacatccca 425  
Db 361 AGCATCTATCAGGCACTCTGAGCTTCTGTACAACGAGTATATAGTGTACAACACAGCTCA 302  
QY 426 ggtgaagatcagttctgtcgaagtgctgttccatcaccaagagt 472  
Db 301 GGTGAAGATGCACTTCTTGTGTAAGTCAAAATTCCTGTCACAGCGTT 255

RESULT 4  
BE420229 369 bp mRNA EST 24-JUL-2000  
LOCUS WMS04.C11R000101 ITEC WMS Wheat Scutellum Library Triticum aestivum  
DEFINITION cDNA clone WMS04.C11, mRNA sequence.  
ACCESSION BE420229  
VERSION BE420229.1 GI:9418075  
KEYWORDS EST.  
SOURCE bread wheat.  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
; Triticaceae; Triticum.  
REFERENCE 1 (bases 1 to 369)  
AUTHORS Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier

, S., Dubcovsky, J., Feullet, C., Gale, M., Graner, A., Gustafson, P.,  
Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P.,  
Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y.,  
Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M.,  
Sortells, M., Warburton, M. and Wenzel, G.  
International Triticaceae EST Cooperative (ITEC): Production of  
Expressed Sequence Tags for Species of the Triticaceae  
Unpublished (2000)  
Contact: Schuch W  
Zeneca Wheat Improvement Centre, Norwich Research Park  
Colney Lane, Norwich NR4 7UH UNITED KINGDOM  
Tel: 44 1603 250 2600  
Fax: 44 1603 250 699  
Email: wolfgang.schuch@aguk.zeneca.com  
International Triticaceae EST Cooperative (ITEC)  
http://wheat.pw.usda.gov/genome.

FEATURES source  
Location/Qualifiers

1. .369  
/organism="Triticum aestivum"  
/cultivar="Novosibirskaya 67"  
/db\_xref="taxon:4565"  
/clone="WMS04.C11"  
/clone\_lib="ITEC WMS Wheat Scutellum Library"  
/tissue\_type="scutellum callus"  
/note="M13 Reverse sequencing primer used for 5' end of  
clone."

BASE COUNT 103 a 78 c 101 g 87 t  
ORIGIN

Query Match 56.8%; Score 269.2; DB 10; Length 369;  
Best Local Similarity 85.2%; Pred. No. 9e-71;  
Matches 312; Conservative 0; Mismatches 53; Indels 1; Gaps 1;  
QY 64 ctaagaattgcaacctctgaggaacctgttactggctatatgttcggcaaaagccctctac 123  
Db 5 CGAGGATAGCACCTCTGAGGCTCTCTGACAGGCTATATGTTGGCAAAAGGCTCTAC 64  
QY 124 ttgcagatctagtaagcaagcgccacaactactgttatgtgataggaataatcctgta 183  
Db 65 TTTGAGATTTAGTAAAGCAAGAGTGCACAGTATTGTTATGTGGATAGAAAAATCCGACT 124  
QY 184 ggttgatgcttcttctgaggtgcttcttaggagacatgtatgaactaaagaagccacg 243  
Db 125 GCCTTGATGCTTCTTCTGAGGTGCTCTAGGAGACATGCATGAACCTGAAAAAGGCCACG 184  
QY 244 tccatggacaaacctccaagaggaagcattcgaccagggattaggcaaaacccgtgcc 303  
Db 185 CCAATGGCAAAACCTCCCAAGAGGAAGCATTCGACCAAGGCTTAGGAAAACTGTGCCG 244  
QY 304 ctggagtcagagtttgaagtgaggatgatgctgtagttccctgcgcaagccggtg 363  
Db 245 CTAGAGTCGGAGTTTGTGAAATGGAGGATGATATCGTCGCTTGTGGCAAGCCAGTG 304  
QY 364 ccatcatcaattaggagctctgaactcatgtacaaatgagtaacatcgtctacacacatcc 423  
Db 305 CCAGCATCTATCAGGCGCATCTGAGCTTCTGT-CAACGAGTATATAGTCTACACACAGCC 363  
QY 424 cagggtg 429  
Db 364 CAGGTG 369

RESULT 5  
BG042229 502 bp mRNA EST 31-JUL-2001  
LOCUS su93c12.y1 Gm-c1055 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
DEFINITION Gm-c1055-2064 5', similar to TR:Q92P54 Q92P54 POLY(ADP-RIBOSE)  
ACCESSION BG042229  
VERSION BG042229.1 GI:12488706  
KEYWORDS EST.  
SOURCE soybean.

ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

REFERENCE 1 (bases 1 to 502)  
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpeliding,J., Coryell,V., Khanna  
A., Bolla,B., Marz,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,  
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers  
Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk  
R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann  
R., Waterston,R. and Wilson,R.  
Public Soybean EST Project  
Unpublished (1999)  
Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available through: Genome Systems, Inc. 4633 World  
Parkway Circle St. Louis, Missouri 63134 For further information  
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)  
427-3324 or contact: clones@genomesystems.com or  
info@genomesystems.com web site: www.genomesystems.com  
Insert length: 429 std Error: 0.00  
High quality sequence stop: 419.

## FEATURES

Location/Qualifiers  
1..502  
/organism="Glycine max"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl055-2064"  
/clone\_lib="Gm-cl055"  
/tissue\_type="Mature seed pods, greenhouse grown"  
/lab\_host="DH10B"  
/note="Vector: pBluescript II SK+; Site\_1: EcoRI; Site\_2:  
XhoI; The cDNA library was constructed from mRNA isolated  
from mature seed pods of greenhouse grown plants prior to  
senescence for the cultivar KPI. Complementary DNA was  
synthesized from mRNA using a primer consisting of a  
poly(dT) sequence with a XhoI restriction site. EcoRI  
adapters were ligated to the blunt-ended cDNA fragments  
followed by XhoI digestion. The cDNA fragments were  
directionally cloned into the EcoRI-XhoI restriction site  
of the pBluescript vector. The ligated cDNA fragments  
were transformed into DH10B host cells (GibcoBRL). This  
library was constructed in the laboratory of Dr. Randy  
Shoemaker."

BASE COUNT 150 a 80 c 119 g 153 t

## ORIGIN

Query Match 39.9%; Score 189; DB 11; Length 502;  
Best Local Similarity 73.0%; Pred. No. 1.8e-46;  
Matches 243; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 140 gcaagcgcaactactgtatgtggataggataatccctgtaggttgatgctttt 199  
DB 2 GCAAAAGTCTCAGTATGCTTCTACTGATAGAAAATCCTGTGGCTAATGCTTTGA 61

QY 200 ctgaggttgccttagagacatgtatgaactaaagaaagccacgtccatggacaacctc 259  
DB 62 GTGAAGTTCGCTTGGAAATGCTATGAGCTCAAGAAAGCTAAGTATATGATAAACCCTC 121

QY 260 caagaggaagcattcgaccaggattaggaacacccgtgccactggagtcaggtttg 319  
DB 122 CGAAGGAAAGCACCTCTACTAAAGGACTGGGCAAGAAAATGCCACAGAAATCGGAATATG 181

QY 320 tgaagtggaggatgatgtcgtagttccctcgccgcaagccggtgcatcatcaatagga 379  
DB 182 TAAAGTGGAGGGCAATGTCACCTGTTCTTGTGGCAACACAGTGCATCAATGTCAGA 241

QY 380 gctctgaactcatgtacaatgagtagcatcgtctacacacatcccaaggtagaagtcagt 439  
DB 242 GTTCTGAGCTCATGTAACATAGTATATGTTTATATACTGCTCAAGTTAAGATGCAAT 301

QY 440 tcttctgtaggtgcgtttccatcaccaagaggt 472  
DB 302 TCTTATTGAAGTGAGGTGTTTCATCACAAGAGAT 334

RESULT 6  
BE941860  
LOCUS BE941860  
DEFINITION BE941860  
ACCESSION BE941860  
VERSION BE941860.1 GI:10519619  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.  
1 (bases 1 to 419)  
Cote,F., Ojanen-Reuths,T., Hahn,M.G., VandenBosch,K., Hur,J.,  
Beremand,P., Endre,G., Town,C.D., Bowman,C.L., Craven,M.B. and Cho  
J., Fraser,C.M.  
ESTs from seedling roots of Medicago truncatula after treatment  
with beta glucan elicitor preparation from Phytophthora sojae  
Unpublished (2000)  
Contact: Michael G. Hahn  
Complex Carbohydrate Research Center  
University of Georgia  
220 Riverbend Road, Athens, GA 30602-4712, USA  
Tel: 706-542-4457  
Fax: 706-542-4412  
Email: hahncrcr.uga.edu  
University of Georgia name: G269712e TIGR sequence name: MTAP09TK  
More information is available at: http://chrysie.tamu.edu/medicago  
Seq primer: SKmod (CTA gaa CTA gtg gat CC).

FEATURES  
Location/Qualifiers  
1..419  
/organism="Medicago truncatula"  
/cultivar="A17"  
/db\_xref="taxon:3880"  
/clone="pMGHG-6B18"  
/clone\_lib="MGHG"  
/tissue\_type="Roots from four day old seedlings"  
/dev\_stage="2 days after treatment with beta glucan  
elicitor preparation from Phytophthora sojae"  
/lab\_host="E. coli strain XL0LR"  
/note="Vector: pBluescript SK+; Site\_1: EcoRI; Site\_2:  
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA  
was directionally ligated into the Unizap XR vector from  
Stratagene and packaged using Gigapack III Gold packaging  
extracts. Plasmids containing cDNA inserts were excised  
from the recombinant lambda-Zap phage using Ex-assist  
helper phage and propagated in XL0LR cells."

BASE COUNT 131 a 87 c 101 g 100 t

## FEATURES

Location/Qualifiers  
1..419  
/organism="Medicago truncatula"  
/cultivar="A17"  
/db\_xref="taxon:3880"  
/clone="pMGHG-6B18"  
/clone\_lib="MGHG"  
/tissue\_type="Roots from four day old seedlings"  
/dev\_stage="2 days after treatment with beta glucan  
elicitor preparation from Phytophthora sojae"  
/lab\_host="E. coli strain XL0LR"  
/note="Vector: pBluescript SK+; Site\_1: EcoRI; Site\_2:  
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA  
was directionally ligated into the Unizap XR vector from  
Stratagene and packaged using Gigapack III Gold packaging  
extracts. Plasmids containing cDNA inserts were excised  
from the recombinant lambda-Zap phage using Ex-assist  
helper phage and propagated in XL0LR cells."

BASE COUNT 131 a 87 c 101 g 100 t

Query Match 39.3%; Score 186.2; DB 11; Length 419;  
Best Local Similarity 74.9%; Pred. No. 1.2e-45;  
Matches 233; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1 acaagatgctattatgacacgttcaaggttgacaaattttgtggaattcttagtcaa 60  
DB 109 AACAGAATGCTCCTATGGCATGGTTCCTAGGCTGACGAACCTTTGTGGCATCTTACCAA 168

QY 61 gggctaagaattgcacctcctcgtggcaccctgttactggctatatgttcggcaagcctc 120  
DB 169 GGACTGAGAAATGCACCTCCCGAAGCCCTGCAACTGGTTATATGTTGGCCCAAGGATG 228

QY	121	tactttgcagatctagttaagaagacgcaacaatacttattgttgataggataataacct	180
Db	111		
Db	229	TACTTTGCTGCACCTTGTGCAGAAAGTGCTCAGTATTGCTTCACTGATGAAGAAAATCCT	288
QY	181	gtaggttgatgcttcttctcgaagttgcttttagggagacatgatgaactaaagaaacc	240
Db	111		
Db	289	GCTGGTCATAAGTTTTGATGAAGTTGCCCTTGGAAATGTGTATGAGCTCAAAAAAGCT	348
QY	241	acgtccatgagcaaacctcaaagaggaagcattcgaccaaggagattaggcaaacccgtg	300
Db	111		
Db	349	AAGTATATGATAAACCTCCGAAGGAACCATCTACTAAGGACTGGCGACAAGAAATG	408
QY	301	ccactggagtc 311	
Db	111		
Db	409	CCCTGGGAATC 419	

RESULT	7
AVB33893/c	
LOCUS	661 bp mRNA EST 22-JUN-2001
DEFINITION	AVB33893 K. Sato unpublished cDNA library; Hordeum vulgare subsp. vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA clone rbagsl0f19, mRNA sequence.
ACCESSION	AVB33893
VERSION	AVB33893.1 GI:14525982
KEYWORDS	EST.
SOURCE	Hordeum vulgare subsp. vulgare.
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE	1 (bases 1 to 661)
AUTHORS	Sato,K.
TITLE	Barley EST sequencing project in NIG and Okayama Univ
JOURNAL	Unpublished (2001)
COMMENT	Contact: Kazuhiro Sato Research Institute for Bioresources Okayama University, Barley Germplasm Center Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan Email: kazsato@rib.okayama-u.ac.jp, URL:http://www.rib.okayama-u.ac.jp/barley/ Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct submission; database:http://www.shigen.nig.ac.jp/barley/Barley.html.

FEATURES	Location/Qualifiers
source	1..661
	/organism="Hordeum vulgare subsp. vulgare"
	/cultivar="Haruna Nijo"
	/db_xref="taxon:112509"
	/clone="rbagsl0f19"
	/clone_lib="K. Sato unpublished cDNA library; Hordeum vulgare subsp. vulgare shoots germination"
	/tissue_type="shoots"
	/dev_stage="germination"
BASE COUNT	183 a 179 c 133 g 164 t 2 others
ORIGIN	

Query Match	34.1%; Score 161.4; DB 10; Length 661;
Best Local Similarity	61.9%; Pred. No. 4.6e-38;
Matches 293; Conservative	0; Mismatches 171; Indels 9; Gaps 2;

QY	1	aacaagatgcattatggcacggttcgaagttacgaattttgtggaaattcttagtcaa	60
Db	633	AACAGATGCTTTTATGGCATGTTCCTGGCTGCTAACCTGGCTGGGATATTTTCTCAG	574
QY	61	ggcctaagaattgcacctctcaggcacctgttactggctatatgttcgccgaagcctc	120
Db	573	GGTTTGGAATTGCTCTCTCTGAAGCGCCTGTTACTGGCTACATGTTTGAAGGGCGTT	514
QY	121	tactttgcagatctagttaagaagacgcaacaatacttattgttgataggataataacct	180
Db	111		

Db	513	TACTTGGCCGATATGTTCTCCAAAGACTGCAAACTACTGCTATGCTTCCAAACACTCTAGA	454
Qy	181	gtaggtttgatgcctctttcttaggtggtcttttagggagacatgatgaactaagaaagcc	240
Db	453	TCTGGGTGCTGCTTCTATGTGAGGTTGCAC TGGGAGACATGAATGAAC TACTAGATGCA	394
Qy	241	acgtccatgg---acaaacctcccaagaggaagcattcgaccacaaggagattaggcaaaac	297
Db	393	AAGTAGCATGCTTAATTAACCTGCCCAAGGAAACTAAGTACTAAGGGAGTTGGCCAGATG	334
Qy	298	gtccactagatccagagtttgaagtgaaggatgatgtcgtagttccctcgcgcaag	357
Db	333	GCACACGCGGAGTCGAAGTCAACCGA-----GGATGGCGTCTGTGTTCCATCTCGAANA	280
Qy	358	ccggtgccatccatcaattaggagctctgaactcatgataatgagtacatcgctctacaac	417
Db	279	CCCAAGAAGAACCTTCAAAGAGGGGTAGCTGCTGTACAACAGGTACATTGTTACAAC	220
Qy	418	acatcccaggtagaagatgcagttctctgctgaagggtcgctttccatccacaagag	470
Db	219	GTAGAGCAGATCAGGATGCGGTACGTGCTCCATGTTTCCCTTTAACTTCAAGGG	167
RESULT	8		
D42790			
LOCUS	D42790	442 bp mRNA	EST
DEFINITION	D42790	Rice callus cDNA (H.Uchimiya) Oryza sativa	CDNA clone 285,
ACCESSION	D42790		
VERSION	D42790.1	GI:3107055	
KEYWORDS	EST.		
SOURCE	Oryza sativa.		
ORGANISM	Oryza sativa		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
TITLE	Enharctoideae; Oryzeae; Oryza.		
JOURNAL	1 (bases 1 to 442)		
COMMENT	Uchimiya,H. On nucleotide sequence of Oryza sativa Unpublished (1994) Contact: Hirofumi Uchimiya Institute of Mol. & Cell. Bioscience, Department of Cellular Function The University of Tokyo 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113, Japan Tel: 03-3812-2111(ex.7844) Fax: 03-3812-2910 Email: huchimiya@tansei.cc.u-tokyo.ac.jp PROJECT= Uchimiya.		
FEATURES			
source	Location/Qualifiers		
	1..442		
	/organism="Oryza sativa"		
	/db_xref="taxon:4530"		
	/clone="285"		
	/clone_lib="Rice callus cDNA (H.Uchimiya)"		
	/tissue_type="callus"		
BASE COUNT	126 a 89 c 110 g 111 t	6 others	
ORIGIN			
Query Match	32.9%;	Score 155.8;	DB 11; Length 442;
Best Local Similarity	76.8%;	Pred. No. 1.9e-36;	
Matches	239;	Conservative 0;	Mismatches 63; Indels 9; Gaps
Qy	171	gataatacctgtaggtttgatg--cttcttcttgaggtgtgttttagggagacatgtatgaa	228
Db	1	GAATAAACCCAGTNGNTTATGCCCTCTCTCCCAAGGTTGCCGCCAGTNNACATGTATGAA	60
Qy	229	ct--aaagaaagccagctccatggacaaa-cctccaagaggaagcattccaccagaagg	284
Db	61	CNTGAAGAAAGGCCACCGCATGGACAACCTCTCAAGAGGGAACACTCGACCCAAAG	120
Qy	285	attaggcacaaa---ccqgtgccactgaggtcagagtttgtgaagtggagggtatgttgt	341

Query Match	34.1%	Score 161.4;	DB 10;	Length 661;
Best Local Similarity	61.9%;	Pred. No. 4.6e-38;		
Matches 293; Conservative	0;	Mismatches 171;	Indels	9; Gaps 2;

Oy	1	aacaagatgcattatggcgcggttcaaggcttgacgaattttgtgggaattcttagtcaa	60
Dd	633	AACAGGATGCTTTTATGGCATGTGCCGCCTGTCFAACTGGCTGGGATATTTCCTCAG	574
Oy	61	gggctaagaattcacactcctgaggcacctytttactggctatatgttcggcgaaggctc	120
Dd	573	GGTTTGAGAATTGCTCTCCTGAAGCGCCGTGTTACTGGCTACATGTTTGGAAAGGGCGTT	514
Oy	121	tactttgcagatcatagttaagcaagagcgacaaatactgttatgtgataggaataatccct	180

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Query Match      32.9%; Score 155.8; DB 11; Length 442;
Best Local Similarity 76.8%; Pred. No. 1.9e-36;
Matches 239; Conservative 0; Mismatches 63; Indels 9; Gaps
4

QY 171 gaataatcctgtaggtttgatg--ctctcttcttgaggtgtgcttaggagacatgatgaa 228
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GAAAAACCCAGTNGNTTTTATGCCCTCTTCCCAAGGTTGCCCCCAAGTNACATGATGAA 60

QY 229 ct---aaagaagccagctccatggacaaa-ctctcaagaagggaagcatctgcaccaagg 284
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CNTGAAGAAGAGCCCAAGCCGCGCATGGACAAACCCCTCCAAAGAGGGAACACATCGACCCCAAG 120

QY 285 attaggcaaaa----ccgtgccactgaagtcadagattttgaaagtggagggatgatgttgt 341

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Db 121 NCTTAGGCAAAACCCGTCGCGCTCAGTCTCAGTTTCGGAATGAGGAGTATGTTGT 180
Qy 342 agtctccctgcagcagcggtgcacatcaatagagagctgaactcatgtacaatga 401
Db 181 GTGCGCATGCGGAAGCAGGCGCCAGCATCTATCAAGACATCTGAGCTTATGTACAATGA 240
Qy 402 gtacatcgtctacaacacatcccaggtgaagatgcagttcttctgctgaaggtgcgtttcca 461
Db 241 GTATATTGTTTCAATACATCCAGGTCAAGATGCGAGTACCTGTTGTAAGGTTAGGTCCA 300
Qy 462 tcacaagaggt 472
Db 301 TCACAAGAGGT 311

RESULT 9
BI217470 716 bp mRNA EST 11-JUL-2001
LOCUS 602933675F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5096850 5',
DEFINITION mRNA sequence.
ACCESSION BI217470
VERSION BI217470.1 GI:14670914
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 716)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11232 row: f column: 19
High quality sequence stop: 696.
FEATURES
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Location/Qualifiers
1..716
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5096850"
/lab_host="NCI_CGAP_Li9"
/clone_lib="NCI_CGAP_Li9"
/Note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: This is a NCI_CGAP Library."
BASE COUNT 175 a 196 c 191 g 154 t
ORIGIN
Query Match 32.1%; Score 152.2; DB 11; Length 716;
Best Local Similarity 59.3%; Pred. No. 2.8e-35;
Matches 278; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

Qy 1 aacaagatgctattatggcagcaggttcacaggttgacgaattttgtggaaattcttagtcaa 60
Db 12 AACCGAGGCTGCTGTGCGCAGGCTCCAGGACACACACCTTGTGCGCATCTCTCCGAG 71
Qy 61 gggctagaagtgcacctctcaggacacctgttactggtctatgttctgcgaagagcctc 120
Db 72 GGTCTCGGATAGCCCCACCTGAAGCGCGCTGTGACAGGCTACATGTTTGGGAAAGGGATC 131
Qy 121 tactttgcagatctagtgaagcagagggcacaatactgttatgttggaataaatacct 180

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Db 132 TACTTTGCCGACATGTTGTCCTCAAAAGTGCAAACTACTGCCACACATCTCTCAGGAGACCCG 191
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Db 192 ATTGGCTTATATACTGCTGGGAGAGGTTCCTTGGAAACATGTATGAACATCAAGCATGCT 251
Qy 241 acgtccatggacaaacctccaagagggagcattccacaaagggattagggcaaaaccgctg 300
Db 252 TCACATATCAGCAAGTTACCCAAGGCGCAAGCAGGTGTCAAGAGTTTGGGAAAAACC --- 308
Qy 301 ccaactgagcagatgttgaagtgaagggatgctgtatgttccctgcggcagagccg 360
Db 309 ACCCTGACCTTCGCCAGCATCACCTGGAGGGGTAGAGGTTCCACTGGGAACAGGG 368
Qy 361 gtgccatcatcaattagtaggagctctgaactcatgtacaatgagtcacgtctacaacaca 420
Db 369 ATCCCATCTGCTCAACGACACCTGCCCTGCTGTATATAGTACATTTGCTACGACATT 428
Qy 421 tccacgtggaagtgcagttcttctgctgaaggtgcgtttccatcacaaga 469
Db 429 GCTCAGGTGAATCTCAATACCTGCTGAAACTCAAGTTCATTTTAAGA 477

RESULT 10
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LOCUS 601662539F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3962696 5',
DEFINITION mRNA sequence.
ACCESSION BE911127
VERSION BE911127.1 GI:10408111
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 587)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9129 row: n column: 09
High quality sequence stop: 559.
FEATURES
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Location/Qualifiers
1..587
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3962696"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/Note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 149 a 163 c 150 g 125 t
ORIGIN
Query Match 31.8%; Score 150.6; DB 11; Length 587;
Best Local Similarity 59.1%; Pred. No. 8.1e-35;
Matches 277; Conservative 0; Mismatches 189; Indels 3; Gaps 1;

Qy 1 aacaagatgctattatggcagcaggttcacaggttgacgaattttgtggaaattcttagtcaa 60

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Db 25 AACGGAGGCTGTGGCAGCGCTCAGGACCAACCACTTTGCTGGCATCTCTGTGCGCAG 84
Qy 61 gggctgaagaattgcacctctcctgagccacctgttactggtatgtatgttgcgaagcctc 120
Db 85 GGTCTGGGATAGCCCACTGAGCGCTGTGACAGGCTACATGTTTGGAAAGGGATC 144
Qy 121 taatttcagatctagtaagcaagagcgacacatactgttattgtgdataggaataatcct 180
Db 145 TACTTTGCCACATGTGTCCAAAGTGAACACTACTGCCACACATCTCAGGAGACCGC 204
Qy 181 gtaggttgatgtttcttctgaggtgtttaggagacatgtatgaacataaagaagcc 240
Db 205 ATTGGCTTAATACTGTGGGAGAGGTGCGCTTGGAAACATGTATGAACATCAAGCATGCT 264
Qy 241 acgtccatgacacaaacctccaagaggaagcattcgaccaaaggtatagcgaagcgtg 300
Db 265 TCACATATCAGCAAGTTACCAAGGCAAGCAGTGTCAAGGTTTGGGAAACACCC--- 321
Qy 301 ccactggagtcagagttgtgaagtgaggagtgatgtcgttagttccctgcggcaagcgg 360
Db 322 ACCCTTGACCTTCGCCAGCATCACCTGGAGGGGTGTAGAGGTTCCACTGGGAACAGGG 381
Qy 361 gtccatcatcaattaggagctctgaactcatgtacataagtagtacctctcacaaca 420
Db 382 ATCCCATCTGGTGTCAACGACACCTGCGCTGTATCATATGATGATACATTTCTACGACATT 441
Qy 421 tccagagtgaaagtcagttctgttgaaagtggtgcgtttccatcacaaga 469
Db 442 GCTCAGGTGAATCTCAATACCTGCTGAACACTCAAGTTCAATTTTAAGA 490

RESULT 11
BI079902
LOCUS 602876096F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5007983 5',
DEFINITION BI079902 725 bp mRNA EST 20-JUN-2001
ACCESSION BI079902
VERSION BI079902.1 GI:14498232
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 725)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Incyte Genomics, Inc.
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M11051 row: o column: 24
High quality sequence stop: 664.
Location/Qualifiers
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/organism="Mus musculus"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5007983"
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/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DHI08"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

FEATURES
source
1. 725
/organism="Mus sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2988216"
/clone_lib="NIH_MGC_15"

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ORIGIN
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Best Local Similarity 59.4%; Pred. No. 8.7e-35;
Matches 274; Conservative 0; Mismatches 184; Indels 3; Gaps 1;

Qy 9 gctattatggcagcggttcaaggttgacgaattttgtgggaattcttagtcaagggctaaag 68
Db 2 GCTGTGTGGCAGCGCTCCAGGACCAACTTTGCTGGCATCTCTGTGCGAGGCTCTCGC 61
Qy 69 aattgcacctctcctgagggcaccctgttactggttatgttcggcaaaagccctctactttgc 128
Db 62 GATAGCCCCACCTGAAGCGCCTGTGCACAGGCTACATGTTTGGGAAAGGGATCTACTTTGC 121
Qy 129 agatctagtaagcagcgcacatactgttattgtgtgtaggaataatcctcttagtttt 188
Db 122 CGACATGTTGTCCTCAAAAGTGAACACTACTGCCACACATCTCAGGAGACCCGATTGGCTT 181
Qy 189 gatccttcttctgaggttgcctttaggagacatgtatgaacataaagaagccacgtccat 248
Db 182 AATACGTGCTGGGAGAGGTGCGCTTGGAAACATGTATGAACATCAAGCATGCTTCACATAT 241
Qy 249 ggacaaacctccaagaggaagcattcgaccaaaggtatagcgaagcgtgcacatgga 308
Db 242 CAGCAAGTTACCAAGGCAAGCAGTGTCAAGGTTTGGGAAACACCC---ACCCCTGA 298
Qy 309 gtccagagttgtgaagtgaggagtgatgtcgttagttccctgcggcaagcgggtgcacatc 368
Db 299 CCCCTTCGCCAGCATCACCTTCGAGGGGTGTAGAGGTTCCACTGGGGAACAGGATCCCATC 358
Qy 369 atcaattaggagctctgaaactcatgtacatgaatgaatgaatcctctcacaacatccacgt 428
Db 359 TGGTGTCAACGACACCTGCGCTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 418
Qy 429 gaagatgcagttctgtggaagtggtgcgtttccatcacaaga 469
Db 419 GAATCTCAAAATACCTGCTGAACACTCAAGTTCAATCTTTAAGA 459

RESULT 12
BI0304535
LOCUS 601105502F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988216 5',
DEFINITION BI0304535 571 bp mRNA EST 13-JUL-2000
ACCESSION BI0304535
VERSION BI0304535.1 GI:9175756
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 571)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW77 row: c column: 01
High quality sequence stop: 567.
Location/Qualifiers
1. 571
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2988216"
/clone_lib="NIH_MGC_15"

FEATURES
source
1. 571
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2988216"
/clone_lib="NIH_MGC_15"

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Db 365 ATAGGCTTAATCCTGTTGGGAGAAAGTTGCCCTTGGAAACATGTATGAACCTGAAGCAGCT 424  
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 Db 425 TCACATATCAGCAAGTTACCCCAAGGGCAAGCACAGTGTCAAAGGTTTGGGCAAAACTACC 484  
 Qy 301 ccaactggagtcagagattttgtgaagtggaggagatgatgtcgtagttccctgcggaagccg 360  
 Db 485 CCTGATCCTTCAG---CTAACATTAGTCTGGATGGTGTAGACGTTCCTCTTGGGACCCGGG 541  
 Qy 361 gtgcacatcatcaatattaggagctctgaactcatgtacaaatgagtagcatcgtctacaacaca 420  
 Db 542 ATTTTCATCTGGTGTGAATGACACACCTCTCTACTATATACGAGTACATTGTCTATGATATT 601  
 Qy 421 tcccagggtgaagatgcagttcttgcgaaggtgcggtttccatcacaaga 469  
 Db 602 GCTCAGGTAATCTGAAGTATCTGCTGAACCTGAAATTCAAATTTAAGA 650

Search completed: March 7, 2002, 15:24:30  
 Job time: 3340 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2002, 14:32:50 ; Search time 4873.04 Seconds  
(without alignments)  
9983.538 Million cell updates/sec

Title: US-09-236-995D-1  
Perfect score: 2949  
Sequence: 1 atggcgccgcgcaaggc.....gtttccatcacagaaggttag 2949

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 1472140 seqs, 8248589755 residues  
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

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- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.om.\*
- 20: em.or.\*
- 21: em.ov.\*
- 22: em.pat.\*
- 23: em.ph.\*
- 24: em.pl.\*
- 25: em.ro.\*
- 26: em.sts.\*
- 27: em.sy.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htgo\_hum.\*
- 31: em.htgo\_inv.\*
- 32: em.htgo\_rod.\*
- 33: em.htg\_hum.\*
- 34: em.htg\_inv.\*
- 35: em.htg\_rod.\*
- 36: em.htg\_other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2797.6	94.9	3285	8	AF093627	AF093627 Zea mays
2	2720	92.2	3211	8	ZMPARP2	ZMPARP2 Zea mays
3	1060.2	36.0	3187	8	ATH131705	ATH131705 Arabidops
4	249.4	8.5	3036	5	GGPADPRP	GGPADPRP Chicken mRN
5	245.8	8.3	3589	4	BOVPAS	BOVPAS Bovine poly
6	239.2	8.1	3718	5	XELPADPRP	XELPADPRP Frog mRNA f
7	238.2	8.1	3617	5	XLPARPG	XLPARPG X.laeviss PA
8	224.6	7.6	3640	9	HUMPOLP	M18112 Human poly(
9	224.6	7.6	3792	6	A52134	A52134 Sequence 1
10	224.6	7.6	3795	9	HUMRISAD	J03473 Human poly(
11	223	7.6	1771	9	HUMADPPO	M17081 Human place
12	222.2	7.5	3047	10	AF168781	AF168781 Cricketsu
13	219.8	7.5	1939	10	RNPARP2	X65497 R.norvegicu
14	219.8	7.5	3045	6	AX058340	AX058340 Sequence
15	219.8	7.5	3045	6	AX062277	AX062277 Sequence
16	219.8	7.5	3660	9	HUMPOL	M32721 Human poly(
17	219.8	7.5	3747	6	I14359	I14359 Sequence 5
18	217.4	7.4	3128	10	RNU94340	U94340 Rattus norv
19	217.2	7.4	3845	10	BC012041	BC012041 Mus muscu
20	216	7.3	1732	10	AF126717	AF126717 Mus muscu
21	212.4	7.2	3172	10	MMADPRP	X14206 Mouse mRNA
22	205.2	7.0	3200	6	AX058362	AX058362 Sequence
23	204.4	6.9	2147	8	ATPARP	Z48243 A.thaliana
24	204.2	6.9	3463	3	SPEPADPRP	D16482 Sarcophaga
25	200.2	6.8	2295	8	ZMPARP1	AJ222588 Zea mays
26	191.8	6.5	1754	9	HS236912	AJ236912 Homo sapi
27	191.8	6.5	1814	6	AX058317	AX058317 Sequence
28	191.8	6.5	1843	6	AX008892	AX008892 Sequence
29	191.8	6.5	1874	6	AX058374	AX058374 Sequence
30	191.6	6.5	3080	3	DROADPREA	D13806 Fruit fly m
31	190.2	6.4	1797	9	HS236876	AJ236876 Homo sapi
32	190.2	6.4	1910	9	AF085734	AF085734 Homo sapi
33	186.2	6.3	121158	2	AP003889	AP003889 Oryza sat
34	185.4	6.3	1980	9	AK001980	AK001980 Homo sapi
35	183.2	6.2	1822	3	DMPARP5	AF051548 Drosophil
36	183.2	6.2	10988	2	AC014613	AC014613 Drosophil
37	183.2	6.2	16864	3	AE002892	AE002892 Drosophil
38	179.8	6.1	1707	6	AX058338	AX058338 Sequence
39	179.8	6.1	1707	10	MMU7780	AJ007780 Mus muscu
40	179.8	6.1	1766	10	AF072521	AF072521 Mus muscu
41	175.8	6.0	79663	8	AC006593	AC006593 Arabidops
42	171	5.8	864	6	AX058336	AX058336 Sequence
43	163.8	5.6	687	6	AX058382	AX058382 Sequence
44	163.8	5.6	738	6	AX058380	AX058380 Sequence
45	163.2	5.5	5787	9	GORADPRB	L24094 Gorilla gor

ALIGNMENTS

RESULT 1

AF093627	AF093627	3285 bp	mRNA	PLN	29-NOV-1998
LOCUS	Zea mays	poly(ADP)-ribose polymerase (PARP1)	mRNA	complete cds.	
DEFINITION	Zea mays	poly(ADP)-ribose polymerase (PARP1)	mRNA	complete cds.	
ACCESSION	AF093627				
VERSION	AF093627.1	GI:3928870			
KEYWORDS					
SOURCE	Zea mays.				
ORGANISM	Zea mays				
REFERENCE	1 (bases 1 to 3285)				
AUTHORS	Mahajan,P.B. and Zuo,Z.				
TITLE	Purification and cDNA cloning of maize Poly(ADP)-ribose polymerase				
JOURNAL	Plant Physiol. 118 (3), 893-905 (1998)				
MEDLINE	99026291				
REFERENCE	2 (bases 1 to 3285)				
AUTHORS	Mahajan,P.B. and Zuo,Z.				
TITLE	Direct Submission				



[illegible]

Qy	2638	gtgataggaataatcctgttagtttgcatttccttcttgagggttgcttttagggagaacatg	2697
Db	2731	GTGATAGGAATAAATCCTTCTAGTTTGATGCTCTCTTTCTGAGGTTCGTTTAGGAGACAATG	2790
Qy	2698	tatgaactaaagaaaagccacgtcccatggacaaaaacctccaagaggaagcattcgaccaag	2757
Db	2791	TATGAACTAAGAAGAACCCACGCTCATGGACAAACTCCAAGAGGGAACATTCGACCACAG	2850
Qy	2758	ggattaggcaaaaaccgtgccactggagtccagagtttgtgaagtggaggatgatgtcgtta	2817
Db	2851	GGATTAGCAAAAACCGTGCCACTGAGTTCAGAGTTTGTGAAAGTGAGGAGATGATGTCGTA	2910
Qy	2818	gttccttcgcgaagccggtgccatcatcataatgaagcctctgaactcatctacaatgag	2877
Db	2911	GTTCCCTCGCACAACCGCGTGCCATCAATAGGAGCTCTGAACTCATGTACAATGAG	2970
Qy	2878	tacatcgtctacaacacatcccaggtgaagatgcagttcttctgtaaagtgcgttccat	2937
Db	2971	TACATCGTCTACAACACATCCAGGTGAAGATGCAGTTCTTGCTGAAGTGCGTTTCCAT	3030
Qy	2938	cacaagaggtgag	2949
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RESULT#	2		
ZMPARP2			
LOCUS	ZMPARP2	3211 bp	mRNA PLN 19-NOV-1997
DEFINITION	Zea mays mRNA for poly(ADP-ribose) polymerase (3211bp).		
ACCESSION	AJ222589		
VERSION	AJ222589.1	GI:2632128	
KEYWORDS	PAP gene; poly(ADP-ribose) polymerase.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	Babychuk E., Cottrill P., Storozhenko S., Fuangthong M., O'Farrell M., Van Montagu M., Inze D. and Kushnir S.		
TITLE	Higher plants possess two poly(ADP-ribose) polymerases		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3211)		
AUTHORS	Kushnir S.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-NOV-1997) Kushnir S., VIB, Dep.Genetics, Ledeganckstraat 35, Gent, B9000, Belgium		
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CDS	113..3022		
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RESULT 3  
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 LOCUS  
 DEFINITION Arabidopsis thaliana mRNA for poly(ADP-ribose) polymerase.  
 ACCESSION AJ131705

VERSION AJ131705.1 GI:4038490  
 KEYWORDS NAD(+) ADP-ribosyltransferase; parp-1 gene; poly(ADP-ribose) polymerase.  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 REFERENCE 1 (bases 1 to 3187)  
 AUTHORS Kazmaier,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-DEC-1998) Kazmaier M., Departement D'Ecophysiologie Vegetale Et De Microbiologie, Commissariat A L'energie Atomique, CEA Cadarache, Lab. De Radiobiol. Vegetale, Bat. 185, 13108 St. Paul-les-Durance, FRANCE  
 REFERENCE 2 (bases 1 to 3187)  
 AUTHORS Doucet-chabeaud,G. and Kazmaier,M.  
 JOURNAL Unpublished  
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Query Match 36.0%; Score 1060.2; DB 8; Length 3187;  
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## RESULT 4

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GGPADPRP 3036 bp mRNA VRT 12-SEP-1993
LOCUS Chicken mRNA for poly(ADP-ribose) polymerase (EC 2.4.2.30).
DEFINITION X52690
ACCESSION X52690
VERSION X52690.1 GI:63742
KEYWORDS NAD(+) ADP-ribosyltransferase.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 3036)
Direct Submission
TITLE Ittel, M.E.
JOURNAL Submitted (30-MAY-1990) Ittel M.-E., Centre de Neurochimie du
C.N.R.S., 5 Rue Blaise Pascal, 67084 Strasbourg Cedex, France
2 (bases 1 to 3036)
Ittel, M.E., Garnier, J.M., Jeltsch, J.M. and Niedergang, C.P.
Chicken poly(ADP-ribose) synthetase: complete deduced amino acid
sequence and comparison with mammalian enzyme sequences
Gene 102 (2), 157-164 (1991)
JOURNAL 91340148
MEDLINE
COMMENT Data kindly reviewed (27-AUG-1990) by Niedergang C.
FEATURES Location/Qualifiers

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 LOCUS Bovine poly(ADP-ribose) synthetase (EC 2.4.2.30) mRNA.  
 DEFINITION D90073 GI:217581  
 ACCESSION DNA binding protein; helix-turn-helix; nuclear location signal;  
 VERSION poly(ADP-ribose) synthetase; zinc-binding finger motif.  
 KEYWORDS Bovine thymus, cDNA to mRNA, clone pSO-7.  
 SOURCE Bos taurus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 3589)  
 AUTHORS Saito, I., Hatakeyama, K., Kido, T., Ohkubo, H., Nakanishi, S. and  
 Ueda, K.  
 TITLE Cloning of a full-length cDNA encoding bovine thymus

# JOURNAL COMMENT

poly(ADP-ribose) synthetase: evolutionally conserved segments and  
 their potential functions  
 Gene (1990) In press  
 These data kindly submitted in computer readable form by: Isao  
 Saito  
 Department of Clinical Science and Laboratory Medicine Faculty of  
 Medicine, Kyoto University  
 Shogoinkawahara-cho 54, Sakyo-ku  
 Kyoto 606  
 Japan  
 Phone: 075-751-3467  
 Fax: 075-771-4792  
 Zinc-binding finger motifs are observed in seq. 21-51 and 128-165.  
 The sequences, 200-220 and 250-270, showed helix-turn-helix  
 structure. Nucleotide-binding fold was found in seq. 890-903.

## FEATURES source

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Query Match 8.3%; Score 245.8; DB 4; Length 3589;  
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 VERSION Z12139  
 KEYWORDS poly(ADP-ribose) polymerase.  
 SOURCE African clawed frog.  
 ORGANISM  
 Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 Xenopodinae; Xenopus.  
 1 (bases 1 to 3617)  
 AUTHOR Saulier-le Drian, B.M.  
 JOURNAL Thesis (1992) Lab. de Biol. et Genet. du Developpement, Universite  
 de Rennes I. URA CNRS 256  
 REFERENCE 2 (bases 1 to 3617)  
 AUTHORS Saulier-le Drian, B.M.  
 TITLE Direct Submission  
 JOURNAL  
 FEATURES  
 Location/Qualifiers  
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gene

CDS



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3'UTR  
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BASE COUNT 1131 a 757 c 910 g 819 t  
ORIGIN

Query Match 8.1%; Score 238.2; DB 5; Length 3617;  
Best Local Similarity 51.7%; Pred. No. 2.4e-50;  
Matches 700; Conservative 12; Mismatches 602; Indels 39; Gaps 7;  
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LOCUS Human poly(ADP-ribose) polymerase mRNA, complete cds.  
DEFINITION M18112  
ACCESSION M18112.1 GI:190166  
VERSION polymerase.  
KEYWORDS Human SV40 transformed fibroblast, cDNA to mRNA, clone pPAP.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 3640)  
Uchida,K., Morita,T., Sato,T., Ogura,T., Yamashita,R., Noguchi,S.,  
Suzuki,H., Nynuya,H., Miwa,M. and Sugimura,T.  
TITLE Nucleotide sequence of a full-length cDNA for human fibroblast  
poly(ADP-ribose) polymerase  
JOURNAL poly(ADP-ribose) polymerase  
MEDLINE Biochem. Biophys. Res. Commun. 148 (2), 617-622 (1987)  
COMMENT 88076933  
Draft entry and computer readable sequence for [1] kindly provided  
by K.Uchida, 02-MAR-1988.  
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BASE COUNT 999 a 833 c 1008 g 800 t  
ORIGIN Chromosome lp11-qter.

Query Match 7.6%; Score 224.6; DB 9; Length 3640;  
Best Local Similarity 51.1%; Pred. No. 7.8e-47;  
Matches 693; Conservative 11; Mismatches 612; Indels 39; Gaps 7;  
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Db 3136 GAAGTATCTCTGAACTGAAATTCAAATTTAAGA 3170

RESULT 9  
A52134  
LOCUS A52134 3792 bp DNA PAT 11-MAR-1997  
DEFINITION Sequence 1 from Patent WO9618737.  
ACCESSION A52134  
VERSION A52134.1 GI:2304739  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 3792)  
AUTHORS Buerkle, A., Zur, H. H. and Kuepper, J.  
TITLES VECTORS AND VIRUSES FOR USE IN GENE THERAPY  
JOURNAL Patent: WO 9618737-A 1 20-JUN-1996;  
DEUTSCHES KREBSFORSCH (DE)  
FEATURES  
Source location/Qualifiers  
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 BASE COUNT 1048 a 846 c 1035 g 863 t  
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 QY 1842 ttatgtgttaaaagacacca-----aaacggaaagatatcagtgaaatgaaagttc 1895  
 DB 2024 CTATGGCCAGGATGAAGAGGACGTGAAGAAGCTGACAGTAAATCCTGGCCACCAGTCCAA 2083  
 QY 1896 tctgtccctcaattgtagaactcatgaagatgcttttcaatgtggagacatatagac 1955  
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 DB 2144 AGCCATGTGGAGTATGAGATCGACCTTCAGAGATGCCCTTGGGAAGCTGAGCAAAAG 2203  
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 DB 2204 GCAGATCCAGGCGCATACTCCATCTCTAGTGGTCCAGGTCAGAGCGCGT-----GTCTCAG 2258  
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 DB 3089 GAAGTATCTGCGTGAAGTGAATTCATTTTAAAGA 3123

RESULT 10  
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 LOCUS Human poly(ADP-ribose) synthetase mRNA, complete cds.  
 DEFINITION J03473  
 ACCESSION J03473.1 GI:337423  
 VERSION poly(ADP-ribose) synthetase.  
 KEYWORDS Human placenta, cDNA to mRNA (library of H.Okayama), clones  
 SOURCE PPARS[1,11,21,32,32,41,-F].  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 3795)  
 AUTHORS Kurosaki,T., Ushiro,H., Mitsuuchi,Y., Suzuki,S., Matsuda,M.,  
 Matsuda,Y., Katunuma,N., Kangawa,K., Matsuo,H., Hirose,T.,  
 Inayama,S. and Shizuta,Y.  
 TITLE Primary structure of human poly(ADP-ribose) synthetase as deduced  
 from cDNA sequence  
 JOURNAL J. Biol. Chem. 262 (33), 15990-15997 (1987)  
 MEDLINE 88058958  
 COMMENT Draft entry and printed copy of sequence for [1] kindly provided by  
 Y.Shizuta, 23-NOV-1987.  
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[illegible]

old sequence

old\_sequence

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Query Match 7.6%; Score 224.6; DB 9; Length 3795;  
Best Local Similarity 51.1%; Pred. No. 7.8e-47;  
Matches 693; Conservative 11; Mismatches 612; Indels 39;

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Qy	1722	tgaggcaatcaagggaattccaaagattattcttgagaagacttgaaactcatgtggaagc	1781
Db	1919	GGATGCCATTAGCAGCTTCATGAATTTATGAAGAAAAACCCGGAAACGCTTGGCACTC	1978
Qy	1782	ttgggaatgaaaaaccaattttcgaagacgcctggagattttaccacttcaatgttga	1841
Db	1979	C-----AAAATTTCCAGNAGTATCCCAAAAGTTCTACCCCTGGAGATTGA	2026
Qy	1842	ttatggtgttaagaagcacc-----aaacggaagatcatcagtgaaatgaaaagttc	1895
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Qy	1896	tctgtcctcctaattgctagaactcatgaagatgcttttcaattgagacatatagagc	1955
Db	2087	GCTCCCAAGCCAGTTCAGGACCTCATCAAGATGATCTTTGATGTGAAAGTATGAAGAA	2146
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Db	2147	AGCCATGTTGGAGTATGAGTCGACCTTTCAGAAGATGCCCTTGGGGAAGCTGAGCAAAAG	2206
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Db	2207	GCAGATCCAGGCCGCGATACTCCATCCTCAGTGGAGGTGCAGACGCGGT-----GTCTCAG	2261
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RESULT 11  
HUMADPO

HUMADPRO  
LOCUS

LOCUS

### DEFINITION

ACCESSION

VERSION

## KEYWORDS

**KEYWORDS**  
**SOURCE**

SOURCE  
ORGANIC

## ORGANISMS

11

## REFERENCES

## AUTHORS

## NOTES

— 100 —

[illegible]

RESULT 11	
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LOCUS	HUMADPPO 1771 bp mRNA PRI 30-OCT-1994
DEFINITION	Human placental poly(ADP-ribose) polymerase mRNA, partial cds.
ACCESSION	M17081
VERSION	M17081.1 GI:178151
KEYWORDS	.
SOURCE	Human placenta cDNA to mRNA, clone lambda-PAP803.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1320; 1560 to 1771) Suzuki,H., Uchida,K., Shima,H., Sato,T., Okamoto,T., Kimura,T.

**TITLE**  
 Molecular cloning of cDNA for human poly (ADP-ribose) polymerase and expression of its gene during HL-60 cell differentiation [published erratum appears in Biochem Biophys Res Commun 1987 Nov 13;148(3):1549]  
**JOURNAL**  
 Biochem. Biophys. Res. Commun. 146 (2), 403-409 (1987)  
**MEDLINE**  
 87298455  
**REFERENCE**  
 2 (bases 1321 to 1559)  
**AUTHORS**  
 Suzuki, H., Uchida, K., Shima, H., Sato, T., Okamoto, T., Kimura, T. and Miwa, M.  
**TITLE**  
 Errata  
**JOURNAL**  
 Biochem. Biophys. Res. Commun. 148, 1549-1550 (1987)  
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CDS

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AF168781

LOCUS

DEFINITION

AF168781

CDs.

ACCESSION

VERSION

KEYWORDS

AF168781 3047 bp mRNA ROD 28-JUL-1999  
 Cricetulus griseus poly ADP-ribose polymerase (PARP) mRNA, complete  
 AF168781.1 GI:5616519



Db 2994 GAAATACCTGCTGAAGTCAAGTTAAATTTAAGA 3028

## RESULT 13

## RNPAP2

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## source

## CDS

RNPAP2 1939 bp DNA ROD 20-MAY-1992  
R.norvegicus mRNA for poly(ADP-ribose) polymerase (clone pRATC).  
X65497  
X65497.1 GI:56849  
NAD(+) ADP-ribosyltransferase.  
Norway rat.  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 1939)  
Thibodeau, J., Gradwohl, G., Dumas, C., Clairoux-Moreau, S., Brunet, G.,  
Penning, C., Poirier, G. G. and Moreau, P.  
Cloning of rodent cDNA coding the poly(ADP-ribose) polymerase  
catalytic domain and analysis of mRNA levels during the cell cycle  
Biochem. Cell Biol. 67 (9), 653-660 (1989)  
90027702  
2 (bases 1 to 1939)  
Potvin, F.  
Direct Submission  
Submitted (23-MAR-1992) F. Potvin, Molecular Endocrinology, CHUL  
Research Center, 2705, Boul Laurier, Ste-Foy, Quebec, G1V 4G2,  
CANADA  
See also X65496.

Location/Qualifiers

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524 a 468 c 521 g 426 t

## BASE COUNT

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Conservative

## Indels

## Gaps

## Length

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 Christenson, E., Demaggio, A.J., Goldman, P.S. and Mcelligott, D.L.  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: March 7, 2002, 14:35:10 ; Search time 298.35 Seconds  
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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	2720	92.2	3211	21	DNA encoding the p
4	224.6	7.6	3793	17	DNA-binding domain
5	221.8	7.5	3580	20	Human poly(ADP-rib
6	219.8	7.5	3045	22	Human tankyrase2 r
7	205.2	7.0	3200	22	Fusion protein PAR
8	204.4	6.9	2147	21	DNA encoding the p
9	200.2	6.8	2295	21	DNA encoding the p
10	191.8	6.5	1566	22	Human poly(ADP-rib
11	191.8	6.5	1814	22	hparp2 cDNA. Homo

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Poly(ADP-ribose)-p  
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Oligonucleotide D2  
Oligonucleotide D1  
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Oligonucleotide D2  
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Nucleotide sequenc  
Human tankyrase2 e  
Novel human polynu  
Yeast AOD9604-asso  
EST R28562, fragme  
Oligonucleotide D1  
5' end fragment of  
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Nucleic acid encod  
Fragment P2-1 derl  
Fragment P2-9 derl  
Internal control B  
Degenerate DNA seq

#### ALIGNMENTS

RESULT 1

AXX89542  
ID AAX89542 standard; cDNA: 2949 BP.

XX AC AAX89542;

XX DT 06-OCT-1999 (first entry)

XX DE Maize poly ADP-ribose polymerase gene.

XX KW PARP; poly ADP-ribose polymerase; metabolism; maize; transform; ss.

XX OS Zea mays.

XX FH Key Location/Qualifiers

XX CDS

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XX      27-JAN-1998; 98US-0072785.
XX
XX      (PION-) PIONEER HI-BRED INT INC.
XX
XX      Mahajan P, Zuo Z;
XX
XX      WPI; 1999-444613/37.
XX      P-PSDB; AAY28464.
XX
XX      New maize poly ADP-ribose polymerase gene useful in transforming
XX      plants to alter their metabolic state
XX
XX      Claim 1; Page 30-35; 48pp; English.
XX
XX      The sequence is the maize poly ADP-ribose polymerase (PARP) gene. The
XX      sequence codes a PARP with 982 amino acids (AAY28464). PARP is required
XX      in the cell in most cases of DNA repair, recombination, rearrangement
XX      and transposition. PARP gene and antisense gene can be used to transform
XX      plant cells and alter the metabolic state of the transformed cell. This
XX      is useful in enhancing disease resistance in plants and methods of
XX      genetic transformation of plants. Plants transformed with either a sense
XX      or antisense PARP nucleotide sequence may be utilized to increase
XX      transformation frequency in plant cells. The enzyme also plays a role in
XX      cellular stress, so may be beneficial for prevention of plant disease or
XX      pathogen attack.
XX
XX      Sequence 2949 BP; 895 A; 539 C; 732 G; 756 T; 27 other:
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XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 2949; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      |||||
DB      1 atggcgccgcgcgaaggcggtggaagcgagatgccaagtctggcgccgctctgtgc 60
QY      61 aagtcacgcggtccctctatgcgaaggaccagctccgctctgtggcaagatggttcaggcg 120
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QY      241 gagaagatacgaactacgttggagtgctcagctcagctgggtacaaagttctacagctcct 300
DB      241 gagaagatacgaactacgttggagtgctcagctcagctgggtacaaagttctacagctcct 300
QY      301 cctgagaaatgtacaattgagattgctccatctgcccgtacttcgcttagacgatgcagt 360
QY      |||||

```

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DB      301 cctgagaaatgtacaattgagattgctccatctgcccgtacttcgcttagacgatgcagt 360
QY      361 gaaaagattacaaaagatcgcgtccgctcttcagcttaagcttgagagtgaaaggtcccaag 420
DB      361 gaaaagattacaaaagatcgcgtccgctcttcagcttaagcttgagagtgaaaggtcccaag 420
QY      421 ggtataccatggtatcatcgcgaactgtttcttttgagggtatccccctctgcaactgttgag 480
DB      421 ggtataccatggtatcatcgcgaactgtttcttttgagggtatccccctctgcaactgttgag 480
QY      481 aagttctcaggtgggatactttgtccgagtaggagtaagagaaacacatgctcgaattctgtt 540
DB      481 aagttctcaggtgggatactttgtccgagtaggagtaagagaaacacatgctcgaattctgtt 540
QY      541 aaaaagatgttggcaacaataaacaataaggttccaaagcgaagaaagtgaaaaat 600
DB      541 aaaaaga tgttggcaacaataaacaataaaggttccaaagcgaagaaagtgaaaaat 600
QY      601 gatatgtgagctacaaaatcccgcagggttagatgaaagtacatctgaaaggtacagtgcgga 660
DB      601 gatattgagctacaaaatcccgcagggttagatgaaagtacatctgaaaggtacagtgcgga 660
QY      661 acaaaaggcaactgttagaccccagctggttccaaatactagttcagctgatatccaaata 720
DB      661 acaaaaggcaactgttagaccccagctggttccaaatactagttcagctgatatccaaata 720
QY      721 aagcttaaggagcaaaagtacacacactttggaagttaaaggatgaacttaagactaatgta 780
DB      721 aagcttaaggagcaaaagtacacacactttggaagttaaaggatgaacttaagactaatgta 780
QY      781 tcggctgctgaattaaaggagatgcttgaggcctaagtggcaggaatacatcaggaccagaa 840
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QY      901 gctgtgctaagtgcgatctactattataatggtcagtcacacatgcagtggttaagtgtca 960
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QY      1141 agaacatcattgctgtcttcttaaggggttggaataaattaggtttctgttggtaggacaa 1200
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QY      1381 gaattgttaaaagcaaaaatgctccattgattgataaactggaatgccttagag 1440
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 Db 1741 aaaagattattctgaagactggaactcgaactcattggaagcttgggaatgaacaaat 1800  
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 Db 1801 ttccggaagcagcctgggagattttaccacttgattgttattatggtttaagaaagca 1860  
 Qy 1861 ccaaacggaaaagatatcagtgaattgaaagtctctcttctcctcctaatgctagaactc 1920  
 Db 1861 ccaaacggaaaagatatcagtgaattgaaagtctctctcctcctaatgctagaactc 1920  
 Qy 1921 atgaagatgctttcaagtgtgaacatatagactcgtactgatgaatttgaawtaat 1980  
 Db 1921 atgaagatgctttcaagtgtgaacatatagactcgtactgatgaatttgaawtaat 1980  
 Qy 1981 atgtcagaaatgctcttgggaagctgaagcgaactgaatattgagaaagca 2040  
 Db 1981 atgtcagaaatgctcttgggaagctgaagcgaactgaatattgagaaagca 2040  
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 Qy 2281 gataaataatgaacitcactgtgaacatcaccccgctggtcagcagatgaagattac 2340  
 Db 2281 gataaataatgaacitcactgtgaacatcaccccgctggtcagcagatgaagattac 2340  
 Qy 2341 aagtttaattgagcagatctctcctcaacacacatgctcctcactcaaggactggtgcctg 2400  
 Db 2341 aagtttaattgagcagatctctcctcaacacacatgctcctcactcaaggactggtgcctg 2400  
 Qy 2401 gaactggagggaagtttttcaacttgatcagatggagaacttaataagtaactcaagatat 2460  
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 Db 2701 gaactaaagaagccacgtccatgacaaacctccaagagggaagcattcgcaccaagggga 2760  
 Qy 2761 ttaggcaaaacccgtgccactgagtcagagttgtgaagtggaggaatgctgaattc 2820  
 Db 2761 ttaggcaaaacccgtgccactgagtcagagttgtgaagtggaggaatgctgaattc 2820  
 Qy 2821 cctctggcgcaagccggtgccatcacaattagagctctgaactcatgtacaatgagtac 2880  
 Db 2821 cctctggcgcaagccggtgccatcacaattagagctctgaactcatgtacaatgagtac 2880  
 Qy 2881 atcgtctacaacacatccacaggtgaagatgcagttcttctgctgaaggtgcgtttccatcac 2940  
 Db 2881 atcgtctacaacacatccacaggtgaagatgcagttcttctgctgaaggtgcgtttccatcac 2940  
 Qy 2941 aagagtag 2949  
 Db 2941 aagagtag 2949

RESULT 2  
 AA260618  
 ID AA260618 standard; DNA; 3212 BP.  
 XX  
 AC AA260618;  
 XX AC  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE DNA encoding the poly(ADP-ribose) polymerase ZAP2 protein of Zea mays.  
 XX  
 KW ZAP2; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase;  
 KW programmed cell death; apoptosis; growth rate; stress; cold; pathogen;  
 KW pest; drought; heat; fungi; nematode; seed-shatter; ss.  
 XX  
 OS Zea mays.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 81..3023  
 FT /tag= a  
 FT /product= "ZAP2 protein"  
 XX  
 PN WO200004173-A1.  
 XX  
 PD 27-JAN-2000.  
 XX  
 PF 12-JUL-1999; 99WO-EP04940.  
 XX  
 PR 17-JUL-1998; 98US-0118276.  
 XX  
 XX (PLBZ ) PLANT GENETIC SYSTEMS NV.  
 XX  
 XX Babyichuk E, Kushnir S, De Block M;  
 XX WPI; 2000-182436/16.  
 DR P-PSDB; AAY68839.  
 XX  
 PT Modulating cell death, growth and stress resistance in eukaryotes,  
 PT specifically plants, used, e.g. to impart fungus or nematode resistance  
 XX

PS Disclosure: Page 103-108; 126pp; English.

XX The present sequence encodes the ZAP2 protein of Zea mays. This protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as CC poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The ZAP2 polynucleotide CC sequences can be used for modulation of programmed cell death in CC eukaryotic cells. The method is used, specifically in plants, to induce, CC or protect against, programmed cell death, depending on the extent to CC which PARP activity is reduced. Reducing expression of endogenous ZAP CC class PARP only is also used to modulate programmed cell death, to CC increase growth rate and to produce plant cells that are more tolerant CC of stress (cold, chemical treatments, pathogens, pests, drought, heat, CC etc., or during transformation). Particular applications are generation CC of plants that are resistant to fungi or nematodes; are male or female CC sterile; or have better seed-shatter properties. The methods are also CC used to improve growth of transformed plant cells (and derived calli or CC complete plants).

XX Sequence 3212 BP; 974 A; 600 C; 815 G; 823 T; 0 other;

Query Match 94.8%; Score 2796; DB 21; Length 3212;  
Best Local Similarity 98.3%; Pred. No. 0;  
Matches 2902; Conservative 22; Mismatches 16; Indels 12; Gaps 10;

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Qy	61	aagtcacgtccggtccctctatgcgaagcaccagtcctgttgcaagatggttcaggcg	120
Db	141	aagtcacgtccggtccctctatgcgaagcaccagtcctgttgcaagatggttcaggcg	200
Qy	121	tcacagtcgcagcgttcacatccatgtagaaccatgccagtcgacatcttcacgaagaag	180
Db	201	tcacagtcgcagcgttcacatccatgtagaaccatgccagtcgacatcttcacgaagaag	260
Qy	181	aaccagataaaatccgttgacagatgttgaaaggatagatgcacttagatgggatgacaa	240
Db	261	aaccagataaaatccgttgacagatgttgaaaggatagatgcacttagatgggatgacaa	320
Qy	241	gagaagatacgaatacagtcgtggagtgctcagtcagtcagtcagtcagtcagtcagtc	300
Db	321	gagaagatacgaatacagtcgtggagtgctcagtcagtcagtcagtcagtcagtcagtc	380
Qy	301	cctgagaaatgacaattgagatgtccatctgcccagtcacttcacatgacacatgcagt	360
Db	381	cctgagaaatgacaattgagatgtccatctgcccagtcacttcacatgacacatgcagt	440
Qy	361	gaaaagattacaaaagatcggtccgtctcttcagcctaagcttgagagtgaaagtcaccaag	420
Db	441	gaaaagattacaaaagatcggtccgtctcttcagcctaagcttgagagtgaaagtcaccaag	500
Qy	421	ggtatacattggtatcgcacaaactgtttctttgagtgatccccgtctgcaactgttgag	480
Db	501	ggtatacattggtatcgcacaaactgtttctttgagtgatccccgtctgcaactgttgag	560
Qy	481	aagttctcaggtcggtgatactttgctgagatgagatgaagaaccatgctcgatctgtt	540
Db	561	aagttctcaggtcggtgatactttgctgagatgagatgaagaaccatgctcgatctgtt	620
Qy	541	aaaaaagattgttgcaacaatagaacaaaataaggtttccaaagcgcaagaagaagtgaat	600
Db	621	aaaaaagattgttgcaacaatagaacaaaataaggtttccaaagcgcaagaagaagtgaat	680
Qy	601	gatattgatagctacaaatcccgaggttagatgaaagatcacatctgaaagtcagtcgca	660
Db	681	gatattgatagctacaaatcccgaggttagatgaaagatcacatctgaaagtcagtcgca	740
Qy	661	aacaaagggcaactgttagaccacgtgttccaaactagttcagctgatatccaaacta	720
Db	741	aacaaagggcaactgttagaccacgtgttccaaactagttcagctgatatccaaacta	800

Qy	721	aagcttaagagagcaaaagtacacacactttgaaagttaaaagatggacttaagactcatgta	780
Db	801	aagcttaagagagcaaaagtacacacactttgaaagttaaaagatggacttaagactcatgta	860
Qy	781	tcggctgctgaataaaggagatgctgtgaggtcattggcagagatatacaggaaccagaa	840
Db	861	tcggctgctgaataaaggagatgctgtgaggtcattggcagagatatacaggaaccagaa	920
Qy	841	aggacactattgacatcgctgctgcgagatgaatgctatttggagcgtggtcctgcca	900
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Qy	901	gtctgtctaataagcgtactattataatggtcagatcacaatgcagtggttaagtgtca	960
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Qy	961	gagtggtccaagtgtacatactctgccacagaacctgtccggtttaagaagaagtggcaa	1020
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Qy	1021	attccacatggaacaaagaatgaattacattgaagtgttcaaatctcaaaaggttaag	1080
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Qy	1081	aaaccagagaggttcttccaccaatgtcacctgagaaatctggaagtaaaagcaactcag	1140
Db	1161	aaaccagagaggttcttccaccaatgtcacctgagaaatctggaagtaaaagcaactcag	1220
Qy	1141	agaacatcattgctgctctctctaaagggttggaataaattggtttctgtgttagacaa	1200
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Qy	1321	gctgaagtcaggaagcaagggaggtgaagatcaccaattgtgaaggaggtttacattgga	1380
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Qy	1381	gaatgtgtt-aaaaagaacaaatgctgcatgtgattgtataaaact--ggaaatccctta	1437
Db	1461	gaatgtgtt-aaaaagaacaaatgctgcatgtgattgtataaaact--ggaaatccctta	1520
Qy	1438	gagtcctcaaaagggcmgtactgtcactgttaaaagttaaagggccgaggtgctgttcata	1497
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Qy	1738	ttcaaaagattatttcttgagagactggaaactcatggaagcttggaatgttaaaacc	1797
Db	1815	ttcaaaagattatttcttgagagactggaaactcatggaagcttggaatgttaaaacc	1874

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# RESULT 3 AAZ60615

ID AAZ60615 standard; DNA; 3211 BP.

XX AAZ60615;

AC AAZ60615;

XX 16-MAY-2000 (first entry)

XX DNA encoding the poly(ADP-ribose) polymerase ZAP1 protein of Zea mays.

XX ZAP1; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase;  
 KW programmed cell death; apoptosis; growth rate; stress; cold; pathogen;  
 KW pest; drought; heat; fungi; nematode; seed-shatter; ss.

XX Zea mays.

OS Key Location/Qualifiers

PH CDS 113..3022

FT /\*tag= a

FT /product= "ZAP1 protein"

XX WO200004173-A1.

XX 27-JAN-2000.

XX 12-JUL-1999; 99WO-EP04940.

XX 17-JUL-1998; 98US-0118276.

XX (PLBZ ) PLANT GENETIC SYSTEMS NV.

XX Babyichuk E, Kushnir S, De Block M;

XX WPI; 2000-182436/16.

XX P-PSDB; AAY68833.

XX Modulating cell death, growth and stress resistance in eukaryotes,  
 specifically plants, used, e.g. to impart fungus or nematode resistance

XX Example 1; Page 79-84; 126pp; English.

XX The present sequence encodes the ZAP1 protein of Zea mays. This protein  
 is a poly(ADP-ribose) polymerase (PARP) protein (also known as  
 poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed  
 cell death or apoptosis, and is a nuclear enzyme. The ZAP1 polynucleotide  
 sequences can be used for modulation of programmed cell death in  
 eukaryotic cells. The method is used, specifically in plants, to induce,  
 or protect against, programmed cell death, depending on the extent to  
 which PARP activity is reduced. Reducing expression of endogenous ZAP  
 class PARP only is also used to modulate programmed cell death, to  
 increase growth rate and to produce plant cells that are more tolerant  
 of stress (cold, chemical treatments, pathogens, pests, drought, heat,  
 etc., or during transformation). Particular applications are generation  
 of plants that are resistant to fungi or nematodes; are male or female  
 sterile; or have better seed-shatter properties. The methods are also  
 used to improve growth of transformed plant cells (and derived calli or  
 complete plants).

XX Sequence 3211 BP; 968 A; 604 C; 813 G; 826 T; 0 other;

XX Query Match

XX Best Local Similarity 92.2%; Score 2720; DB 21; Length 3211;

XX Matches 2869; Conservative 22; Mismatches 16; Indels 45; Gaps 11;



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Db 2232 ctcatattacaggaatgagatgatttgatcaaaa-gcgaataatgttgagctctcg 2290
QY 2218 caggatattgaaattgcttcaagaatgtagtggcttgatagcagcagtgatgaattcttt 2277
Db 2291 caggatattgaaattgcttcaagaatgtagtggcttgatagcagcagtgatgaattcttt 2350
QY 2278 gatgataaataatgaaactcactgtgacatcaccccgctgctcaagatgaaagt 2337
Db 2351 gatgataaataatgaaactcactgtgacatcaccccgctgctcaagatgaaagt 2410
QY 2338 tacaagttaattgagcagtatctctcaacacacacatgctcttactcaagaagactggtcg 2397
Db 2411 tacaagttaattgagcagtatctctcaacacacacatgctcttactcaagaagactggtcg 2470
QY 2398 ctggaactggagaaatttttcaacttgatgagatgagagaaacttaataagtaactcaaga 2457
Db 2471 ctggaactggagaaatttttcaacttgatgagatgagagaaacttaataagtaactcaaga 2530
QY 2458 tataaaataaactgcatacaagatgctattatggcagcggttcaaggttgacgaatttt 2517
Db 2531 tataaaataaactgcatacaagatgctattatggcagcggttcaaggttgacgaatttt 2590
QY 2518 gtgggaattcttagtcaagggttaagaattgcaacctctctgagcaccctgttactggtctat 2577
Db 2591 gtgggaattcttagtcaagggttaagaattgcaacctctctgagcaccctgttactggtctat 2650
QY 2578 atgttcggaagagcctctacttctgagatctagttaagaagaagcgcacaaactactgttat 2637
Db 2651 atgttcggaagagcctctacttctgagatctagttaagaagaagcgcacaaactactgttat 2710
QY 2638 gtggataggaataactctgtagtttgatgcttcttctgaggttctttaggagacatg 2697
Db 2711 gtggataggaataactctgtagtttgatgcttcttctgaggttctttaggagacatg 2770
QY 2698 tatgaactaaagaaagccagctccatggacaaacccctcccaagagggaagcattcgaccag 2757
Db 2771 tatgaactaaagaaagccagctccatggacaaacccctcccaagagggaagcattcgaccag 2830
QY 2758 ggattaggaacaaacccgctgcaactggatcagagatttggaaagtgagatgctgta 2817
Db 2831 ggattaggaacaaacccgctgcaactggatcagagatttggaaagtgagatgctgta 2890
QY 2818 gtccctgcggcgaagccggtgccaatcatcatcaattaggagctctgaaactcatgataatgag 2877
Db 2891 gtccctgcggcgaagccggtgccaatcatcatcaattaggagctctgaaactcatgataatgag 2950
QY 2878 tacatcgtctacaacacatcccaggtggaagatgcagttcttctgaggtgcgtttcccat 2937
Db 2951 tacatcgtctacaacacatcccaggtggaagatgcagttcttctgaggtgcgtttcccat 3010
QY 2938 cacaagaggtag 2949
Db 3011 cacaagaggtag 3022
```

## RESULT 4

AAT13732

ID AAT13732 standard; DNA; 3793 BP.

XX AC AAT13732;

XX XX

DT 31-OCT-1996 (first entry)

XX DE DNA-binding domain of poly(ADP-ribose) polymerase coding sequence.

XX DE PARP; DNA-binding domain; poly(ADP-ribose) polymerase; gene therapy;

XX KW tumour treatment; DNA repair; over-expression; ss.

XX OS Homo sapiens.

XX XX

XX FH Key

XX CDS Location/Qualifiers

FT 96..3137

```
FT FT /*tag= a
FT FT /product= poly(ADP-ribose)_polymerase
FT FT /note= "PARP"
FT FT 67..1220
FT FT misc_feature
FT FT /*tag= b
FT FT /note= "encodes DNA-binding domain"
```

XX WO9618737-A2.

XX 20-JUN-1996.

XX 15-DEC-1995;

XX 16-DEC-1994;

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Buerkle A, Kuepper J, Zur Hausen H;

XX WPI; 1996-300654/30.

XX P-PSDB; AAR99642.

XX Vectors contg, insert encoding DNA-binding domain of

XX poly(ADP-ribose) polymerase - useful for gene therapy, esp. of

XX tumours

XX Claim 4; Fig 1; 22pp; German.

XX The present sequence encodes a poly(ADP-ribose) polymerase (PARP) contg.

XX a DNA-binding domain (DBD). The DNA fragment from -29 to +1127

XX (nucleotides 67-1220 of this sequence) encoding the DBD can be inserted

XX into vectors which are used for gene therapy. Over-expression of the DBD

XX inhibits the DNA repair function of PARP, so the vectors are useful for

XX gene therapy or tumours, esp. in combination with conventional chemo-

XX and/or radiotherapy.

XX Sequence 3793 BP; 1049 A; 847 C; 1034 G; 863 T; 0 other;

SQ

## Query Match

Best Local Similarity 7.6%; Score 224.6; DB 17; Length 3793;

Matches 693; Conservative 11; Mismatches 612; Indels 39; Gaps 7;

QY 1602 ctactatgtactccagatcattgaacaggatgattggctgagctcagctatttcgttaa 1661

Db 1796 ctactacaagctctctctgaggacgacaggaacacaggtattggatttcaggtc 1855

QY 1662 gtgggagcgggttgaggatgagaaattggaggcgaacacacaggtattggatttcaggtc 1721

Db 1856 ctggggccggtgtgggtacggtgattcggtagcaacaaactggaacagatgccgtccaagga 1915

QY 1722 tgagcgaatcaaggaaattcaaaagattattttcttgagaagactggaacactcaatgggaagc 1781

Db 1916 ggatgccattgagcattctcatgaaatttatgagaaacacccgggaacgcttggcactc 1975

QY 1782 ttgggaattgaaacaaattttcgaagcagctgggagattttaccacttgattgta 1841

Db 1976 c-----aaatttcacgaagtatcccaaaagtctcccccctggagattga 2023

QY 1842 ttatggtgtaagaaagcacc-----aaacggaagatatcagtgaaatgaaagtctc 1895

Db 2024 ctatggccaggtgaaagagcagtgaaagcgtgacagtaaatcctggcaccagtccaa 2083

QY 1896 tttgtctctcaattgctagaaactcatgaaatgttttcaatgttttgagagacatatagagc 1955

Db 2084 gtcccccaagccagttcaggacctcatcaagatgactttgtgtggaagtatgaaga 2143

QY 1956 tgcctatgaggaatttgaaatgaaatgacaaatgctcttcttggaagcgaagcmaggr 2015

Db 2144 agccatgtggagtagatgagacaccttcagaagatgcccttggggaagcgaagc 2203

QY 2016 aaatatgaggaaggtattgaagcattaaactkrgrtacmtrattttattgaaggacacg 2075



Db 2204 gcagatccagccgcgcatactccatccctcagtgagggtccagcagcggt-----gtctcag 2258  
 Qy 2076 ctatcaagcagcgtgctgtgtrgagaaagctnaattgttgytgsgagcmatsyttttc 2135  
 Db 2259 ggcagcagcagctcagatcctggatctcctcaatcgcttttacaccctgatcccccac 2318  
 Qy 2136 actcttatcccttcttctatccatccatattatatacggagtgaggatgtttcatatcaaa 2195  
 Db 2319 gactttgggatgaagaagcctccgctccggaacaatgcaga-----cagtggtcagggcaa 2374  
 Qy 2196 ggcgaataacttgagcctcgcagatattgaaattgctcaa-----agatagttgg 2249  
 Db 2375 ggtggaatcttgacaacctgctgacatcgtgagcaggtggcgtacagtcgtcaggggagg 2434  
 Qy 2250 ctctgatagcagcagtgatgaatctcttgatgataataatataataaacttcactgtgacat 2309  
 Db 2435 gctgatgatagcagcaaggatccctcgtatgcactatgagaagctcaaaactgacat 2494  
 Qy 2310 caccgcgtggctcagatagtgaaattacaaagttaattgagcagatctctctcaaac 2369  
 Db 2495 taaggtggtgacagagattctgaagaagccgagatcatcagaagatgtttaagaacac 2554  
 Qy 2370 acatgctctactcaacagcagctgctgctggaactggaggagttttttcacttgatog 2429  
 Db 2555 tcattgaacacacacacaaatgctgacttggaagtcacgtatctttaaagatagagcg 2614  
 Qy 2430 agatgagaaacttaataagctactcaagatataaaataatctgcatacaagaatctatt 2489  
 Db 2615 tgaagcgaatccagcgtttacaagccctt---aagcagctctcaacccgaagattgct 2671  
 Qy 2490 atggcaggttcaaggtgacgaattttggaatttttagtcaagggtcaagaattgc 2549  
 Db 2672 gtggcaggttcaggaccacaaacttctggtgactctgtccaggtcttcggtatgc 2731  
 Qy 2550 acctctgaggcactgttactggtctatgttcggcaagccctctactcttgcatct 2609  
 Db 2732 ccgcctgaagcgcctgacaggtcacatgtttgtaaggatctcttctgctgacat 2791  
 Qy 2610 agtaagcagagcgcacatactgttatgtgataggaataatctctgagtttgaatct 2669  
 Db 2792 ggtctcaagagtgcacaaactgcatcactgctcaggagaccacaaataggcttaact 2851  
 Qy 2670 tcttctgaggttctttaggagacatgtatgaactaaagaagccacgtccatggacaa 2729  
 Db 2852 gttgggagaagttgctcttggaacatgtatgaactgaagcagcttccacatcatcagcaa 2911  
 Qy 2730 acctcaagaggaagcattcagcaaggttaggcaaaaacccgtgcactggagtcaga 2789  
 Db 2912 gttaccagggcagagcagcagtgtaaaaggttgggcaaaaactaccctgatcctcag- 2970  
 Qy 2790 gttgtgaggtgagggatgctgtagtctccctgcggcagccggtgcctcatcaat 2849  
 Db 2971 --ctaactatgctggtggtgtagacgttctcttggaccgggattctatctggtgt 3028  
 Qy 2850 taggagctctgaactcatgtataatgatactctctacacacatcccaggtgaagat 2909  
 Db 3029 gaatgacacctctactataacagagtaacattgtctatgatattgctcaggtaaatct 3088  
 Qy 2910 gcagttcttctgaaaggtcgctttccatcaaga 2944  
 Db 3089 gaagtatctgctgaaactgaaattcaattttaaga 3123

## RESULT 5

AAZ23799

ID AAZ23799 standard; cDNA; 3580 BP.

XX AAZ23799;

AC AAZ23799;

XX 18-JAN-2000 (first entry)

DE Human poly(ADP-ribose)polymerase cDNA.

XX

Gene therapy; poly(adenosine diphosphate-ribose) polymerase; treatment;  
 PARP; antitumor; nuclear DNA repair; proliferating cell; DNA damage;  
 protection; genomic instability; cancer; prevention; human; ds.  
 Homo sapiens.  
 Key Location/Qualifiers  
 CDS 140..3184  
 FT /\*tag= a  
 FT /product= "poly(ADP-ribose) polymerase"  
 DE19808889-A1.  
 PD 09-SEP-1999.

XX 03-MAR-1998; 98DE-1008889.

XX 03-MAR-1998; 98DE-1008889.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Buerkle A, Meyer R;

XX WPI; 1999-509563/43.

XX P-PSDB; AAY33699.

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New gene therapy vector expressing poly(adenosine  
 diphosphate-ribose)-polymerase for treating or preventing tumors -  
 Claim 4; Fig 1; 12pp; German.

This invention describes a novel vector (A), suitable for gene therapy,  
 which contains a DNA insert (I) that encodes a practically complete  
 poly(adenosine diphosphate-ribose) polymerase (PARP) which has antitumor  
 activity. PARP is a nuclear DNA repair enzyme (activated by strand  
 breakage), that allows recovery of proliferating cells from the toxic  
 effects of DNA damage (caused by alkylating or oxidizing agents or  
 radiation), and protects cells against such damage or other causes  
 of genomic instability. (A) are used for treatment of cancer and for  
 cancer prevention in subjects at high risk (e.g. those with  
 tumor-associated genetic defects). Tumor cells treated with (A) show an  
 increased tendency to die when treated with radiation or chemotherapeutic  
 agent, and in cells that survive this treatment they inhibit genomic  
 instability, so should reduce the likelihood of further development of  
 both malignant cells and resistance to chemotherapy. This sequence  
 encodes the human poly(ADP-ribose) polymerase described in the invention.

Sequence 3580 BP; 986 A; 823 C; 996 G; 775 T; 0 other;

Query Match 7.5%; Score 221.8; DB 20; Length 3580;

Best Local Similarity 51.1%; Pred. NO. 1.1e-54;

Matches 692; Conservative 10; Mismatches 614; Indels 39; Gaps 7;

Qy 1602 ctactatgtactccagatcattgaacaggtgatgggtctgagtcagtcagttatctgtaa 1661

Db 1843 ctactacaagctcagctcttgaggagcagcaaggaacaggtattgattatcaggtc 1902

Qy 1662 gtggggcaggggtggagtgagaaaaattggaggggcaaaaaactggaggagatgtcaaaaac 1721

Db 1903 ctggggcgtgtgggtacgtcatcgtagcaacaactggaacagatgcgtccaagga 1962

Qy 1722 tgaggcaatcaaggaattcaaaagattattcttgagagactggaactggaactcaggaagc 1781

Db 1963 ggtatgcatggagcactctcagaaattatagaagaaaaacccgggaagcgttggcactc 2022

Qy 1782 ttgggaatgtaaaaaccaattttcggagcagcctggagattttaccacttgatgtga 1841

Db 2023 c-----aaaaatttcacgaagtatcccaaaaagtctaccctcggagattga 2070

Qy 1842 ttatggtttaagaagaagcacc-----aaacggaagatatcatgtaaatgaaagttc 1895

Db 2071 ctatggccaggtgaagagcagtgagagagtgacagtaaatcctggcaccacagtc 2130



Qy 1896 tttgtcctcattgtagaactcatgaagatgcttttcaatgtggagacatatagagc 1955  
Db 2131 gctcccagcagtcaggacctcatcaagatgatttggatgaggaaagtatgaagaa 2190  
Qy 1956 tgcattgatgaattgaaatataatgcagaaatgcctcttggaaagctaaagcmaggr 2015  
Db 2191 agccatgttgagtagagacgaccttcagaaagatgccttgggagagctgagcaaaag 2250  
Qy 2016 aaatttgaaagattgaaagcattaaactkrtaamgrattttatttgaagagacag 2075  
Db 2251 gcagatccagcgcgcatcactccatcctcagtgaggtccagtaggcggt-----gtctcag 2305  
Qy 2076 ctatcaagcactgctgtttrgaaagaaatnaattgttgytgsagcmatsyytttttc 2135  
Db 2306 ggcagcagcactcagatcctgagatcctcaaatgcctttitacacctgacccccac 2365  
Qy 2136 actcttacccttcttaccctcactcattatcacgggatgagatgatttcatatcaaa 2195  
Db 2366 gactttggatgaagagcctcctcctgaacatgcaga----cagtgtagagccca 2421  
Qy 2196 ggcgaaatgcttgaagctgcagagatattgaattgttcaaa-----agatagttgg 2249  
Db 2422 ggtgaaatgcttgaaacctgctgacatgcagatgaggtgcctacagctctgctcagggag 2481  
Qy 2250 ctctgacgacagtgatgactctcttgatgataaaatataatgcacttcaactgtgacat 2309  
Db 2482 gctgatgacagcagagatcccatgcctgctcaactatgagagctcaaaactgacat 2541  
Qy 2310 caccctgctgacgacatgtagaagattacaaatgaattgagcagatctcctcaaac 2369  
Db 2542 taagtggtgacagagatcctgaagagccgagatcaggaagtgtttaaagaaac 2601  
Qy 2370 acatcctcactcaagagactgctgcagaaactgaggaagtgttctcacttgatcg 2429  
Db 2602 tcatgacacacacaaatgcgtatgacttggaaatcgcatacttbaagatgagcgc 2661  
Qy 2430 agatggagaacttaataagtaactgaatataaaataatcgtcatacaagatgctatt 2489  
Db 2662 tgaagcgaatccagcgttaaacgcttt--aagcagcttcaaacgagattgct 2718  
Qy 2490 atgcaaggttcaaggttgacgaatttgggaaattttagtaaggcctgaagaattgc 2549  
Db 2719 ttggcaggggtccagagacacacaaacttctgctggatcctgtccaggggtctcggaagc 2778  
Qy 2550 acctcgaagcacttactgctgctatattgctgcaagcctcacttctgacatct 2609  
Db 2779 ccgctgaagcgcgcgtgacgggtacactgtttgtaagggatctatttgcgtgacat 2838  
Qy 2610 agtaagcaagagcgacaaactgttattggtatgaggaataatcctctgaggtttgagct 2669  
Db 2839 ggtctccaagagtccaactactgcatcgtcctcagggagacccaataggcttaactct 2898  
Qy 2670 tcttctgaggttctttaggagacatgtatgaactaaagaaagcaccatccatgagcaa 2729  
Db 2899 gttgggagagttgcttggaaactgtatgaactgaagcagcgttccatcatcagcaa 2958  
Qy 2730 acctcaagaggaagcattcgcacaaaggtattaggaacaaacgtgccaactggagtcaga 2789  
Db 2959 gttacccaagggcagcagcaggtgtaaaaggtttgggcaaaactacccctgactctcag- 3017  
Qy 2790 gtttggaggtgagggatgattgctcctgctgagcgaagcgggtgccatcatcaat 2849  
Db 3018 --ctaactattgcttgaggtgtagacgttctccttctggaacgggatitctcgtggt 3075  
Qy 2850 taggagctgaactatgataaatgagtagacatcgtctcaacacacatccaggtgagat 2909  
Db 3076 gaatgacacctctactatataacagtagacattgtctgatattgtcaggttaactc 3135  
Qy 2910 gcagttcttgcgaaggtgcgtttccatcacaga 2944  
Db 3136 gaagtattcgtgaaactgaaatccaaattttaaga 3170

## RESULT 6

AAF63954  
ID AAF63954 standard; DNA; 3045 BP.

XX AAF63954;

DT 05-APR-2001 (first entry)

Human tankyrase2 related coding sequence SEQ ID NO: 136.

Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;  
inflammatory disorder; ds.

XX Homo sapiens.

XX WO200100849-A1.

XX 04-JAN-2001.

XX 28-JUN-2000; 2000WO-US17827.

XX 29-JUN-1999; 99US-0141582.

XX (ICOS-) ICOS CORP.

XX Christenson E, Demaggio AJ, Goldman PS, McElligott DL;

XX WPI: 2001-102896/11.

XX P-PSDB; AAB66296.

XX New tankyrase2 polypeptides, useful for treating conditions mediated by  
poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,  
inflammatory and autoimmune disorders.

XX Example 2; Page 203-207; 242pp; English.

XX The present invention provides the protein and coding sequence for the  
human tankyrase2 protein. This is found in two different versions,  
designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has  
CC polyADP-ribosylation activity and is involved in the modification of  
CC TRF1, which is a telomere-specific binding protein. The regulation of  
CC telomere length, in which TRF1 has a role, is linked to ageing and  
CC cancer. The sequences are useful in the treatment of cancers and  
CC inflammatory disorders.

XX Sequence 3045 BP; 863 A; 710 C; 851 G; 621 T; 0 other;

Query Match 7.5%; Score 219.8; DB 22; Length 3045;

Best Local Similarity 50.9%; Pred. No. 3.8e-54;

Matches 690; Conservative 11; Mismatches 615; Indels 39; Gaps 7;

Qy 1602 ctactatgtactcagatcattgaacagatgaggtctgagtgctagctatctgtaa 1661

Db 1704 ctactcaagctgcagctctctgagagcagaaggaacagglattggtattcaggtc 1763

Qy 1662 gtgggagcgggtggagtgagaaattggagggcaaaactggagagatgtcaaaac 1721

Db 1764 ctggggccgtgtgtgacgtgacgtgtagcaaaactggaacagatgcgtccaagga 1823

Qy 1722 tgaggcaatcaagaattcaaaagattattcttgagaagactggaaactcatgggaagc 1781

Db 1824 ggaagcattgagcagttcgaattatgaagaaaaaacgggaacgttggcactc 1883

Qy 1782 ttgggaatgaaaacaaattttcggagcagcctggagattttaccacttgaattga 1841

Db 1884 c-----aaatttcacgaagtatcccaaaagttttacccctggagattga 1931

Qy 1842 ttatgtgttaagaaagcacc-----aaacggaaagatatcagtgaaatgaaagttc 1895

Db 1932 ctatggccaggatgaagagcagtggaagagctcacagtaaatcctctggcaccagttcaa 1991



CC antagonists which may be used to treat a human having a disorder  
 CC mediated by PAR2 activity, such as, inflammatory, neurological,  
 CC cardiovascular, or neoplastic tissue growth disorders. hPAR2 and  
 CC antibodies to it, can also be used to diagnose these conditions.

XX Sequence 3200 BP; 923 A; 745 C; 870 G; 662 T; 0 other;

Query Match 7.0%; Score 205.2; DB 22; Length 3200;

Best Local Similarity 49.9%; Pred. No. 8.2e-50;

Matches 675; Conservative 9; Mismatches 634; Indels 36; Gaps 6;

Qy 1602 ctactatgtactcagatcattgaacagatgatggcttgagctacgtatttcgtaa 1661  
 Db 1812 ctactacaagctgagctcttgaggagcagcaagaaacacaggtatggatcaggtc 1871  
 Qy 1662 tggggagcgggtggagtgagaaatggaggcgaacaaactggagagatgtcacaac 1721  
 Db 1872 ctggggccgctgtgggtacgggtgacgtagcaacaaactggaacagatgcccgtccaaaga 1931  
 Qy 1722 tgaggcaatcaaggaaattcaaaagattattttctggagagactggaaactcatgggaagc 1781  
 Db 1932 ggatgccattgagcattcatgaaattatgaagaaacacgggaacgcttgccactc 1991  
 Qy 1782 ttgggaatgtaaaacaaattttcgaag-----cagcctgggagattttacccacttga 1835  
 Db 1992 caaaaatttcacgaagtatcccaaaagtctacccctggagattgactatgcccagga 2051  
 Qy 1836 tgttattatgtgttaagaaagcaccacaaacggaaagatatcagtgaaatgaaaagtgc 1895  
 Db 2052 tgaagaggcagtgaaagactgacagttaactctggcaccacacgcttccagagtcaca 2111  
 Qy 1896 tctgtctctcaattgctgagactcatgaagatgttttcaatgtggagacataLagagc 1955  
 Db 2112 gctagatctcgggtacagaggttaataaagttgatctgtatgtctcagggccatggaaga 2171  
 Qy 1956 tgcctatgatgaattgaaataatgtcagaataatgcctcttgggaagcctaagcmaggr 2015  
 Db 2172 aatgagtgagaaatgaagtaataaccagaagaagccctcttgggaagctgacagtgc 2231  
 Qy 2016 aatattgagagatttgaagcattaaactrrgtacmrrattttatttgaaggacacgc 2075  
 Db 2232 gcaaatcaagcaggttaccagctctcttaagaagattgaggtatttctcgggtggcca 2291  
 Qy 2076 ctatcaagcacctggttcttgagaaagcnaattgttgytgsagcmatsytttttc 2135  
 Db 2292 gcatgacgagctctcatggaagcatgcaatgaattcta-----caccagagattcc 2342  
 Qy 2136 actcttatccctctattctctcatattatatacgggagtaggagtagatttcattcaaa 2195  
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Db 2694 gcatggtccaggatgagtaactgggtgggaatcttgagccatggcttcgaattgcccc 2753  
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 Db 2874 atcagaggtagctctaggtcagtgtaataactactactagagggccaatcctaaagccgaag 2933  
 Qy 2733 t-----ccaagaggaagcattcgaccacaggttaggcaaaacccgtgccactggagtcaga 2789  
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 Qy 2790 gtttg-----tgaagtgaggagatgatgtcgtagttccctcggcgaagccggtgccatc 2843  
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## RESULT

AAZ60617  
 ID AAZ60617 standard; DNA; 2147 BP.

AC AAZ60617;

DT 16-MAY-2000 (first entry)

DE DNA encoding the poly(ADP-ribose) polymerase NAP protein.

XX NAP; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase;  
 KW Programmed cell death; apoptosis; growth rate; stress; cold; pathogen;  
 KW pest; drought; heat; fungi; nematode; seed-shatter; ss.

OS Arabidopsis thaliana.

FH Key Location/Qualifiers

FT CDS 129..2042

FT /\*tag= a

FT /product= "NAP protein"

XX WO200004173-A1.

PN 27-JAN-2000.

XX 12-JUL-1999; 99WO-EP04940.

XX 17-JUL-1998; 98US-0118276.

XX (PLBZ ) PLANT GENETIC SYSTEMS NV.

XX Babyichuk E, Kushnir S, De Block M;

XX WPI; 2000-182436/16.

XX P-PSDB; AAY68835.

PT Modulating cell death, growth and stress resistance in eukaryotes,  
 PT specifically plants, used, e.g. to impart fungus or nematode resistance

XX Disclosure; Page 95-99; 126pp; English.

Query Match	6.9%	Score 204.4	DB 21	Length 2147
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2019	tattggaagaaggtttgaagcattaaactkrgtacmgttratttatittgaaggaacacgcgt	2078		
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2496	cggttcaaggttgacgaatttttggaatactcttagtcaaggctcaagaattgcacctcc	2555		
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2616	caagagcgcacaaactactgtattggttaggataaataactctgtaggtttgatgccttttc	2675		
1706	caagagtgcgaactatgctatgcacactggcgcgttaatgagtggtctctctctctg	1765		

RESULT	9
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ID	AAZ60616
XX	XX
AC	AAZ60616
XX	XX
DT	16-MAY-2016
XX	XX
DE	DNA error
XX	XX
KW	NAP: F
KW	program
KW	post:
XX	XX
OS	Zea mays
XX	XX
FF	Key
FT	CDS
FT	FT
FT	FT
XX	XX
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PD	PD
XX	27-JAN-2017
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PF	12-JUL-2016
XX	XX
PR	17-JUL-2016
XX	XX
PA	(PLB2)
PI	Baby
XX	XX
DR	WPI: 2
XX	P-PSDB
PT	Modula
PT	specific
PT	Exempl
XX	XX
CCC	The pro
CCC	is a poly
CCC	poly(A) t
CCC	cell de
CCC	sequen
CCC	eukaryo
CCC	or pro
CCC	which i
CCC	class I
CCC	increa



5

Db	1272	cttatacgaaggtagctctaggtcagtgtaatgaactactagagccaatctctaaggccga	1331
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Db	1332	aggattgcttcaagttaaacatagcaccacaagggtggcgaagatggctccagttctgc	1391
QY	2787	aaagtttg-----tgaagtgaggagatgatgtcgtgatttccttgcgcgaagccgtgcc	2840
Db	1392	ccacttcgtccacctgaatggagtagcagtgccattaggaccagcaagtgacacaggaat	1451
QY	2841	atcatcaattagagctctgaactcatgtacaaatgagtacatcgtctacacacatccca	2900
Db	1452	tctgaatccagatggttataccctcaactacaatgaatatattgtatatacccccaacca	1511
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AAC85303  
ID AAC85303 standard; cDNA; 1814 BP.

AAC85303;

XX  
DT 29-MAR-2001 (first entry)XX  
DE  
hpärp2 cdNA.

Human, poly(ADP-ribose) polymerase; hPARP2; oxidative stress; ARDS; inflammation; ischaemic stroke; hemorrhagic shock; myocardial ischemia; infection; cerebral vasospasm; rheumatoid arthritis; osteoarthritis; gouty arthritis; spondylitis; Behcet's disease; sepsis; septic shock; endotoxic shock; gram negative sepsis; gram positive sepsis; trauma; toxic shock syndrome; multiple organ injury syndrome; vasculitis; hemorrhage; conjunctivitis; uveitis; thyroid-associated ophthalmopathy; eosinophilic granuloma; asthma; chronic bronchitis; allergic rhinitis; chronic obstructive pulmonary disease; silicosis; reperfusion injury; pulmonary sarcoidosis; pleurisy; alveolitis; pneumonia; myocardium; bronchiectasis; pulmonary oxygen toxicity; keloid formation; brain; scar tissue formation; atherosclerosis; systemic lupus erythematosus; autoimmune thyroiditis; multiple sclerosis; Reynaud's syndrome; graft versus host disease; allograft rejection; cystic fibrosis; chronic glomerulonephritis; inflammatory bowel disease; Crohn's disease; ulcerative colitis; necrotizing enterocolitis; inflammatory dermatitis; contact dermatitis; atopic dermatitis; psoriasis; urticaria; fever; myalgia; meningitis; encephalitis; Sjogren's syndrome; alcoholic hepatitis; bacterial pneumonia; hypovolemic shock; Type 1 diabetes mellitus; hypersensitivity; leukocytic dyscrasia; thermal injury; cytokine-induced toxicity; ds.

Homo sapiens.

Key	Location/Qualifiers
CDS	63..1814
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T	/product= "hPAPP2"
T	

WO200077179-A2.

X  
D  
21-DEC-2000

16-JUN-2000; 2000WO-US16629.

X  
R 16-JUN-1999; 99US-0139543.

X  
A (ICOS-) ICOS CORP.

Christenson E, Demaggio AJ, Goldman PS, McElligott DL;

WPI; 2001-025335/03.

P-PSDB; AAB47029.

[illegible]













Fri Mar 8 08:31:51 2002

us-09-236-995d-1.rng

Page 20







US-08-044-618-4  
; Sequence 4, Application US/08044618  
; Patent No. 549605  
; GENERAL INFORMATION:  
; APPLICANT: SKULSON, MARK  
; TITLE OF INVENTION: METHOD OR DETECTING A PREDISPOSITION TO  
; TITLE OF INVENTION: CANCER BY THE USED OF RESTRICTION FRAGMENT LENGTH  
; TITLE OF INVENTION: POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE)  
; TITLE OF INVENTION: POLYMERASE  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1225 Connecticut Suite 300  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/044,618  
; FILING DATE: 19930406  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/257,696  
; FILING DATE: 14-OCT-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FOX, SAMUEL L  
; REGISTRATION NUMBER: 30,353  
; REFERENCE/DOCKET NUMBER: 0654.0490001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)466-0800  
; TELEFAX: (202)833-8716  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1592 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-044-618-4

Query Match 4.4%; Score 131; DB 1; Length 1592;  
Best Local Similarity 56.1%; Pred. No. 4.6e-29;  
Matches 288; Conservative 0; Mismatches 220; Indels 5; Gaps 2;  
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DB 1054 CAGAGATCTCGAAGAGCTGAGATCATCAGGAAGTATGTTAAGAACACTCATCGAACCAA 1113  
QY 2382 tcacaggaactgctgcgtggaactgaggaagtttttccacttgatcgaga---tgga 2438  
DB 1114 CCACACAGCATG--CATATGACTTGGAGTCATGATGATGATGATGATGATGATGATGATG 1171  
QY 2439 acttaataagtagtactcaagataataaaataatctgatacaagatgctattggcaagg 2498  
DB 1172 GGAGTGCCAGCAGCTACAGCCCTTTTAAGCAGGCTTCATACTGAAGGTTGCTGTGGCATGG 1231  
QY 2499 ttcaaggttgacgaatttttggaattcttagtcaagggtctaaagattgacccctcga 2558  
DB 1232 GTCCAGGACCACCACTTGTCTGGGATCTGTCCCTGGGCTCTTTGGATAGCCCTGCCTGA 1291  
QY 2559 ggcactgttactggtctatgttcggcaaggccctctactttgagatcttagtaagcaa 2618  
DB 1292 AGCACCTGTGATGGGCTACATGTTTGGTAAAGTGATCTATTTCGCTGATCTTGTCTCCAA 1351

QY 2619 gagcgacaaactgttatgttgataggaataactcctgtagatgcttcttcttctga 2678  
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RESULT 5  
US-09-328-111-216/c  
; Sequence 216, Application US/09328111  
; Patent No. 6262333  
; GENERAL INFORMATION:  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Steinmann, Kathleen E.  
; APPLICANT: Astle, Jon H.  
; APPLICANT: Burgess, Christopher C.  
; APPLICANT: Bushnell, Steven E.  
; APPLICANT: Carroll III, Eddie  
; APPLICANT: Catino, Theodore J.  
; APPLICANT: Derti, Adnan  
; APPLICANT: Ford, Donna M.  
; APPLICANT: Lewis, Marcla E.  
; APPLICANT: Monahan, John E.  
; APPLICANT: Schlegel, Robert  
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
; FILE REFERENCE: CCD-257 (US)  
; CURRENT APPLICATION NUMBER: US/09/328,111  
; CURRENT FILING DATE: 1999-06-08  
; EARLIER APPLICATION NUMBER: US 60/088,801  
; EARLIER FILING DATE: 1998-06-10  
; NUMBER OF SEQ ID NOS: 850  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 216  
; LENGTH: 595  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(595)  
; OTHER INFORMATION: n = A,T,C or G  
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DB 290 TGAGCCATGGGCTTCGAATTCGCCACCTGAAGTCCCATCAGAGTTACATGTTGGGA 231  
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DB 230 AAGGAATCTACTTGTCTGACATGTCTTCCAAGAGTGCGCAATTAAGTCTTCTGCTCT 171  
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; NAME/KEY: 1..375
; LOCATION: 1..375
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; OTHER INFORMATION: Light chain region"
US-08-759-804A-59

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QY 1517 atactgtcacattcctttragnatggaaagcatatatacaatgcameccttaaacatgttc 1576
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QY 1577 tgacct 1582
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Job time: 8137 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 7, 2002, 14:28:50 ; Search time 2934.5 Seconds  
(without alignments)  
10798.876 Million cell updates/sec

Title: US-09-236-995D-1  
Perfect score: 2949  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 22703874

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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4: em\_estom:\*  
5: em\_estpl:\*  
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7: em\_estro:\*  
8: em\_estov:\*  
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10: gb\_estl:\*  
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12: gb\_hc:\*  
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19: em\_gss\_rod:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	484.6	16.4	714	10	AV833309
3	338.2	11.5	607	11	BF255013
4	312	10.6	536	10	BE419432
5	301.8	10.2	427	10	BE516130
6	299	10.1	661	10	AV834168
7	269.2	9.1	369	10	BE420229
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11	186.2	6.3	759	13	AQ577141
12	181	6.1	669	10	AA401836

13	180.8	6.1	861	11	BG280821
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15	170.8	5.8	990	11	BG031594
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17	162.2	5.5	632	11	BG429402
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23	155.4	5.3	716	11	BI217470
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25	153.2	5.2	560	11	BF042005
26	152.6	5.2	771	11	BG751755
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32	148.2	5.0	579	10	AA397988
33	148.2	5.0	792	11	BG533818
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35	147	5.0	924	11	BG259918
36	145.8	4.9	709	10	BE382739
37	145.6	4.9	851	11	BG698037
38	140.8	4.8	928	11	BG675913
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VERSION		AW066305.1	GI:6021377		
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REFERENCE		1 (bases 1 to 653)			
AUTHORS		Walbot, V.			
TITLE		Maize ESTs from various cDNA libraries sequenced at Stanford			
JOURNAL		University			
COMMENT		Unpublished (1999)			
		Contact: Walbot V			
		Department of Biological Sciences			
		Stanford University			
		855 California Ave, Palo Alto, CA 94304, USA			
		Tel: 650 723 2227			
		Fax: 650 725 8221			
		Email: walbot@stanford.edu			
		Plate: 687009, row: D column: 02.			
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## FEATURES

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/organism="Zea mays"	
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/dev_stage="14, 21, 28, and 35 days after pollination"	
/lab_host="E. coli SOLR"	

/note="Organ: embryo; Vector: pBluescript SK; Site\_1: xhoI  
; Site\_2: EcoRI; Library was prepared by Stratagene using  
the Uni-ZAP XR system (Stratagene BN937328-12). Clones  
were picked by a Q-bot after blue/white selection  
(ampicillin resistance - use 100 micrograms/microliter).  
developed from a pool of equal amounts of RNA from  
pollinating embryos sampled at 14, 21, 28 and 35 days after  
pollination of the Illinois High Oil Maize Strain Cycle  
90. This closed strain has been selected for high oil  
concentration for 90 generations and originates from the  
1890s era open pollinated variety Burr's White"

BASE COUNT 215 a 98 c 161 g 178 t 1 others  
ORIGIN

Query Match 19.7%; Score 579.8; DB 10; Length 653;  
Best Local Similarity 96.0%; Pred. No. 7.3e-139;  
Matches 616; Conservative 16; Mismatches 6; Indels 4; Gaps 4;

QY 1601 gctactatgtactccagatcatgaacagagatgggtctgagtgctacgtatttcgta 1660  
DB 16 GCTACTATGTACTCCAGATCATGAACAGGATGATGGTCTGAGTGTACGTATTTCGTA 75

QY 1661 agtgggacggttgagtgagaaatggaggcacaactggagagatgtcaaaaa 1720  
DB 76 AGTGGGACGGGTTGGGAGTGAGAAATTTGGAGGCGCAAAACTGGAGGAGATGTCAAAA 135

QY 1721 ctgaggaatcaagaatcaaaagattattcttgagagactggaaactcatggaag 1780  
DB 136 CTGAGGCAATCAAGGAATTCAAAAGATTATTTCTTGAGAGACTGGAAACTCATGGAAG 195

QY 1781 ctgggaatgtaaaacaaattttcggagcagcctgggagattttaccacttgatgtg 1840  
DB 196 CTGGGAATGTAAACCAATTTTCGGAAGCAGCCTGGGAGATTTTACCACCTGATGTTG 255

QY 1841 attatgggttcaagaagcaccacaaacggaagatatcatggaatgaaagtctcttg 1900  
DB 256 ATTATGGGTGTTAAGAAAGCACCACCAACGGAAGATATCAGTGAATGAAAGTTCTCTTG 315

QY 1901 ctctcaattctggaactcatgaagatgcttttcaatgtggagacatatagagctgcta 1960  
DB 316 CTCCTCAATTCCTAGACTCATGAAGATGCTTTTCAATGTGGAGACATATAGAGCTGCTA 375

QY 1961 tgatggaattgaaatgaaatgcaaaatgctcttggaagctaaagcagaaata 2020  
DB 376 TGATGGAATTTGAATTAATATGTCAGAAATGCTCTTTGGGAAGCTTAAGCAAGCAATA 435

QY 2021 ttgaggaagattggaagcattaaactkrgrtcmgratttattggaagcacccgctnat 2080  
DB 436 TTGAGAAAGGATTTGAAGCATTTAACTGAGATACAGAAATTTA-TTGAAGGACACCGTGAT 494

QY 2081 caagcactgctgttggagaagcnaattgttgytgagcmatssytttttcaactct 2140  
DB 495 CAAGCACTGGC-TGTTAGAAAAGCTTAATTTGTGTGCGAGCAATCGCTTTTCACTCT 553

QY 2141 tatectcttattcactctcatattacagggatgagatgttcatatcaaaagcga 2200  
DB 554 TATCCCTTCTATT-ATNCTCATATTATACGGGATGAGGATGATTTGATGATCAAA-GCGA 611

QY 2201 aaatgctgagctctgcaggatattgaaattgcttcaaga 2242  
DB 612 AAATGCTTGAAGCTCTGCAGGATATTGAAATTTGCTTCAAGA 653

RESULT 2  
AV833309 714 bp mRNA EST 22-JUN-2001  
LOCUS AV833309 K. Sato unpublished cDNA library: Hordeum vulgare subsp.  
DEFINITION vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA  
clone bags5k04, mRNA sequence.  
ACCESSION AV833309  
VERSION AV833309.1 GI:14525398  
KEYWORDS EST.

SOURCE ORGANISM  
Hordeum vulgare subsp. vulgare.  
Hordeum vulgare subsp. vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
; Triticeae; Hordeum.  
1 (bases 1 to 714)

REFERENCE Sato, K.  
Barley EST sequencing project in NIG and Okayama Univ  
Unpublished (2001)  
CONTACT: Kazuhiro Sato  
Research Institute for Bioresources  
Okayama University, Barley Germplasm Center  
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan  
Email: kzsato@rib.okayama-u.ac.jp,  
URL: http://www.rib.okayama-u.ac.jp/barley/  
Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct  
submission:  
database: http://www.shigen.nig.ac.jp/barley/Barley.html.

FEATURES  
source  
1..714  
/organism="Hordeum vulgare subsp. vulgare"  
/cultivar="Haruna Nijo"  
/db\_xref="taxon:112509"  
/clone="bags5k04"  
/clone\_lib="K. Sato unpublished cDNA library: Hordeum  
vulgare subsp. vulgare shoots germination"  
/tissue\_type="shoots"  
/dev\_stage="germination"  
BASE COUNT 249 a 121 c 162 g 182 t  
ORIGIN

Query Match 16.4%; Score 484.6; DB 10; Length 714;  
Best Local Similarity 82.3%; Pred. No. 2.9e-114;  
Matches 587; Conservative 19; Mismatches 102; Indels 5; Gaps 5;

QY 1525 cacattcttgragtggaagacatatacaatgcamcttaaacatgtcttgcacctg 1584  
DB 6 CAGGAGGCTGGAAGATGGCAAAAGCATTTCAATCAACCCCTAAACAT-TTCTGACATGA 64

QY 1585 cacnaggtgtgacaggtctactgtatccagatcattgaacagatgtggtctgag 1644  
DB 65 CACAAGGTGTTAACA-GCTACTATATATCTCAGATCATCGAAGAGATGATGGGAGTGA 123

QY 1645 tgctacgtatttcgaatgggacggttggagtgagaaatggaggcgaactg 1704  
DB 124 TCGTATGATTTTCGAAAGTGGGGGCGAGTTGCCAGTGAAGATTTGGTGAAGAAACTG 183

QY 1705 gaggagatgtcaaaactgaggaatcaatgaagatttcaaaagatttcttgcagaagact 1764  
DB 184 GAGGAGATGTCAAAACCTGACGCAATATACATGAATTTAAAGATTTATTTCTGGAAGACT 243

QY 1765 gaaactcatgggaagcttgggaatgttaaaccatttcggaagcagcctgggagatt 1824  
DB 244 GAAACCCCTGGGAAGCATGGCAACAAAACAAATTTTCAGAACGACCTCGGAGATT 303

QY 1825 laccacttgatgttgattgttgtaagaagcaccacaaacgaaagatatcagtga 1884  
DB 304 TATCCACTTGACATTTGATACGGATTTAAGCAAGCACCAGCAACGAAAGATCATGACAAA 363

QY 1885 atgaaaagtctcttgcctcctcaattgtagaactcatgaagatgcttttcaatgtgag 1944  
DB 364 ATGAAAAGTTCACTTGTCTCTCAGTGTGCAACTCATGATGATGCTTTTCAATGTTGA 423

QY 1945 acatatagactgctatgtagaattgaaatgaataatgtagaagactcctcttgggaag 2004  
DB 424 ACATATAGGCTGCTATGATGGAATTTGAAATCAATATGCGCAAAATGCCCTTGGGAAA 483

QY 2005 ctgaagcaggraaatatttgagagagattggaacttaactkrgrtcmgratttatt 2064  
DB 484 TTAAGCAAGGAAAATATCCAGAAAGGATTTGAAGCATTAATACTGAGATACAAAATCTA-CT 542

QY 2065 gaaggacacgcctnatcaagcactgctgtttrgagaagcnaattgttgytgagcm 2124



2629	Qy	tactgttatgtgtagagaataactcctgtagttgttgatgctctcttcttgagggtgcttta	2688
121	Ddb	TATGTCTATGTGGATAGAAAAATCCGACCTGGCTTGATGCTTCTTCTGAGGTGCTCTA	180
2689	Qy	ggagacatgtatgaactaaagaagccacgtccatgaacaaacctccaaagaggaagcat	2748
181	Ddb	CGAGACATGTCATGAACCTGAAAAAGCAACGCGCAATGGCAAACTCCAGAGGGAAGCAT	240
2749	Qy	tgcaccaagggatagcgcaaaacccgtgacctggagtcagagttgtgaaagtggagggat	2808
241	Ddb	TGACCAAGGGCTTAGGCAGAAACTGTGCCACTAGAGTCGGAGTTGTTAAATGAGGGAT	300
2809	Qy	gatgtcgtagttccctgcggcgcaagccggtgcccatactaatagagctctgaaactcatg	2868
301	Ddb	GATGTCGTGCTGCCCTTGTGGCAAGCAGTCAGCAGCATATCAGGGCATCTGAGCTTCTG	360
2869	Qy	tacaatgagtacatgctctacaacacatcccagctgaagatgcagttcttctgaaagtg	2928
361	Ddb	TACAACGAGTATATAGTTGACAAACACACTCAGGTGAGATGCAGTCTTCTTTGAGGTC	420
2929	Qy	cgtttccatcacaagaggt	2947
421	Ddb	AAATTCCTCACAGGTT	439
RESULT 4			
BE419432			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			

25 microm ABA (abscisic acid) in 5 mM Mes buffer, pH 5.7, for 12 hr at 22 C. The tissue, total RNA, and poly(A) RNA were prepared by Steven Verhey in M.K. Walker-Simmons's lab (USDA-ARS, Washington State Univ., Pullman, Washington 99164-6420. A cDNA library was made by Clontech using a combination of random and oligo dt primers. Library was plated and archived by Russell Johnson (Colby College, ME/Walker-Simmons' lab). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

122 a	93 c	84 q	128 t
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BASE COUNT

[illegible]

dDb	57	ATCTCATACCAAGATGCTATTATGGCATGGTTCAGGCTG	17
RESULT	6		
LOCUS	AV834168/c		
DEFINITION	AV834168	661 bp	mRNA EST
Accession	AV834168	K. Sato unpublished	cdna library: Hordeum vulgare subsp.
Description	vulgare shoots germination	Hordeum vulgare subsp.	vulgare cdna clone rbags5x04, mRNA sequence.
Date	22-JUN-2001		

REFERENCE  
Sato, K. EST sequencing project in NIG and Okayama Univ  
Barley K. (bases 1 to 661)  
Triticaceae; Hordeum.  
TITLE  
Barley K. EST sequencing project in NIG and Okayama Univ  
JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: Kazuhiro Sato  
Research Institute for Bioresources  
Okayama University, Barley Germplasm Center  
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan  
Email: kazsato@rib.okayama-u.ac.jp/  
URL: <http://www.rib.okayama-u.ac.jp/barley/>  
Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct  
submission.





Fri Mar 8 08:31:54 2002

Db 538 TTGAGAGACTGGCACTCATGGAGCATGGCAACAAAAGAAAAATTTTCAGAACCAAC 597  
 Qy 1814 ctggagattttaccacactgatgttgattatgtgttgaagaagaccacaaacggaag 1873  
 Db 598 CTGCAGATTTTCTCTCGATATTGATTTATGGGGTGTGACAAAAAACCACTCTTAAAG 657

Qy 1874 a 1874

Db 658 A 658

## RESULT 10

BG042229 502 bp mRNA EST 31-JUL-2001  
 LOCUS BG042229.1 Gm-cl055 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
 DEFINITION Gm-cl055-2064 5' similar to TR:Q92P54 Q92P54 POLY(ADP-RIBOSE)  
 POLYMERASE ; mRNA sequence.  
 BG042229  
 BG042229.1 GI:12488706

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## BASE COUNT

## ORIGIN

## 150 a

## 80 c

## 119 g

## 153 t

## Shoemaker."

## library was constructed in the laboratory of Dr. Randy

## Shoemaker."

## Shoemaker."

## Shoemaker."

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## Shoemaker."

Query Match 6.4%; Score 189; DB 11; Length 502;

Best Local Similarity 73.0%; Pred. No. 6.3e-38;

Matches 243; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy 2615 gcaagagcgcaacactactgttattgttgtagtaagaataaccccttaggtttgtatgctcttt 2674

Db 2 GCAAAAGTCTCAGTATTCCTTCACTGATGAAGAAAAATCCTGTGCTTAATGCTTTTGA 61

Qy 2675 ctgaggttcttttagggagacatgtatgaactaaaagaagccacgtccatggacaaaccc 2734

Db 62 GTCAAGTTCGGCTTGGAAATGTCTATGAGCTCAAGAAAGCTAAGTATATGGGATAACCTC 121

Qy 2735 caagagggagcatttcgacccaagggattagcaaacccgtgcacactggagtcagagtttg 2794

Db 122 CCAGAAAGAACACCTCTACTAAAGGACTGGGCAAGAAATGCCACAGGAATCGGAATATG 181

Qy 2795 tgaagtggaggatgatgtctgttagtccctcgggcaagccggtgccatcatcaattagga 2854

Db 182 TAAAGTGGAGGGCAATGTCTACTGTTCCTTGTGGCAACACAGTGCCTCAATGTCAAGA 241

Qy 2855 gctctgaactcatgtacaatgaatgactacatcgtctcacacacatcccggtgaagatgca 2914

Db 242 GTTCTGAGCTCATGTCAATGAGTATATGTTTATTAATCTGCTCAAGTAAAGATGCAAT 301

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

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Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

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Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334

Qy 2915 tcttgcgaaggtgcgttccatcatcaagaaggt 2947

Db 302 TCITATTGAAGGTGAGGTTTCATCACAAGAGAT 334



us-09-236-995d-1.rst

Fri Mar 8 08:31:54 2002

```

Qy 2936 atcacaaga 2944
Db 657 ATTTTAAGA 665

RESULT 13
BG280821 861 bp mRNA EST 21-FEB-2001
LOCUS NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4543433 5',
DEFINITION mRNA sequence.
ACCESSION BG280821
VERSION BG280821.1 GI:13029745
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 861)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCML225 row: c column: 18
High quality sequence stop: 825.
Location/Qualifiers
1. .861
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4543433"
/clone.lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: skin; Vector: pOTB7; site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT

ORIGIN

```

Query Match 6.1%; Score 180.8; DB 11; Length 861;
Best Local Similarity 56.0%; Pred. No. 9.4e-36;
Matches 427; Conservative 0; Mismatches 322; Indels 13; Gaps 4;

Qy 2192 caaaggcgaatactgtgaagctctgcagagattgaaattgcttcaa-----agatag 2245
Db 56 CCAAGGTGGAATGCTTGACACCTGCTGGACATCGAGGTGGCTTACAGTCTGCTCAGGG 115

Qy 2246 ttggttcgataggacagatgatgaatctcttgatgataataatgaaacttcactgtg 2305
Db 116 GAGGTCTGATGATAGCAGCAGGATCCCATCGATGTCAACTATGAGAGCTCAAACTG 175

Qy 2306 acatcaccccgctggttcacagatgagattacaaagtttaattgacagatctctca 2365
Db 176 ACATTAAAGTGTGTTGACAGAGATCTTGAAGAACCCGAGATCATCAGGAAGTATGTTAAGA 235

Qy 2366 acacacgtctcctactcaacagactggtcgtcggaactggaggaagtttttcactg 2425
Db 236 ACACCTCATGCAACCCACACACACATCGCTATGACTTGGAAAGTCATCGATATCTTTAAGTAG 295

Qy 2426 atcgagatggagaaacttaataagtaactcaagataataataatctgcatacaagatgc 2485
```

RESULT 14

BI093436

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .916

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone.lib="NIH\_MGC\_10"

/cell\_line="MGC36"

/lab\_host="DH10B"

/note="Organ: cervix; Vector: pCMV-SPORT6; Site:1: NotI;

Site:2: SalI; Cloned unidirectionally. Primer: Oligo dr.

High quality sequence stop: 837.

Location/Qualifiers

1. .916

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone.lib="NIH\_MGC\_10"

/cell\_line="MGC36"

/lab\_host="DH10B"

/note="Organ: cervix; Vector: pCMV-SPORT6; Site:1: NotI;

Site:2: SalI; Cloned unidirectionally. Primer: Oligo dr.

High quality sequence stop: 837.

Location/Qualifiers

1. .916

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone.lib="NIH\_MGC\_10"

/cell\_line="MGC36"

/lab\_host="DH10B"

/note="Organ: cervix; Vector: pCMV-SPORT6; Site:1: NotI;

Site:2: SalI; Cloned unidirectionally. Primer: Oligo dr.



Average insert size 1.5 kb. Library prepared by Life Technologies."	
BASE COUNT	
ORIGIN	
248 a	209 c 230 g 229 t

Query Match	5.9%	Score 174.6	DB 11	Length 916
Best local Similarity	56.4%	Pred. No. 3.8e-34		
Matches 368	Conservative	0	Mismatches 279	Indels 6
Gaps				
2292	gaaaacttcaactgtgaacatcaccccgctggctcagctagtgaagattacaagttaattga	2351		
4	GAAGCTCAAAACTGACATTAAGTGGTTGACAGAGATTCTGAAGAACGCCAGATCATCAG	63		
2352	gcagctatctctcaacacacatctcctcactcaacgaagactggtcgtcgtggaactggagga	2411		
64	GAAATATGTTAAAGAACACTCATGCAACCCACACACAATCGGTATGACTTTGGAAGTCATCGA	123		
2412	agtttttctacttgatcgagatggagaacttaataagttactcaagataataaaaataatct	2471		
124	TATCTTTAAGATAGACGGTGAAGGCCGAATGCCAGCGTTTACAAGCCITTAAGCAG	---CT 180		
2472	gcatacaagatgctattatgycacgggttcaaggttgacgaattttggaatactcttag	2531		
181	TCATACCCGAAGATTGCTGTGSCACGGGTCAGACACCACCAACTTTGCTGGGATCCTGTC	240		
2532	tcaagggtcgaagaattgcacctcctcgtgagccactggttactggcttatgttcggcgaagg	2591		
241	CCAGGGTCTTCGGATAGCCCGCCCTGGAAGCCCGCTGACAGGCTACATGTTTGGTAAAGG	300		
2592	cctctactttgcagatctagLaagcaagagcgcaatactgattatggtataggaaataa	2651		
301	GATCTATTTCGTGCATAGTGGTCTCCAAGAGTGCCAACTACGCCATACGTCTCAGGGAGA	360		
2652	tctgtaggtttgatgcttcttctggagttgcttttaggagacatgtagaactaaagaa	2711		
361	CCCAATAGGCTTAATCTGTGTGGAGAAGTGTGCCCTTGGAAACATGTATGAATGAAGCA	420		
2712	agccacgtccatgacaaacctccaagagggagacattcgaccaaggataggcaaac	2771		
421	CGCTTCACATATACGAAGATTACCCAAGGCAAGCACAGTGTCAAGGTTTGGGCCAAAC	480		
2772	cgtgccactggatcagagtttgtgaagtggaaggatgatgctgtagttccctcgcgcaa	2831		
481	TACCCCTGATCCTTCAG---CTAACATTTAGCTGTGATGGGTGAGACGTTCTCTCTTGGGAC	537		
2832	gcgggtgcacatacaattaggagctctgaaactcagtacatgagtacatcgctctcaa	2891		
538	CGGGATTTTCATCTGGTGTGAATGACACCTCTCTACTATATAACGAGTACATTGTCTATGA	597		
2892	cacatcccagggtgaagatgcagttcttctgaagtgcggtttccatcacaa	2944		
598	TATTGTCTAGGTAAATCTCAAGTATCTGCTGAAACTGAATCTCAATTTTAAAG	65		

RESULT	15	
LOCUS	BG031594	
DEFINITION	603299739F1 NIH_MGC-87 Homo sapiens cDNA clone IMAGE:4394288 5', mRNA sequence.	
ACCESSION	BG031594	990 bp mRNA
VERSION	BG031594.1	EST
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 990)	
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabbs-re@mail.nih.gov">cgabbs-re@mail.nih.gov</a>	

Tissue Procurement: DCTD/DTF  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM10089 row: m column: 09  
 High quality sequence stop: 678.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4394288"  
 /clone\_lib="NIH\_MGC\_87"  
 /tissue\_type="mammary adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: breast; Vector: pCMV-Sport6; Site.1: NotI;  
 Site.2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.383 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."  
 274 a 218 c 251 g 247 t

## FEATURES

Note: this is a NIH\_MGC Library. Sequenced by Life Technologies.

BASE COUNT	274 a	218 c	251 g	247 t
ORIGIN				
Query Match	5.8%;	Score 170.8;	DB 11;	Length 990;
Best Local Similarity	55.7%;	Pred. No. 3.7e-33;		
Matches 389; Conservative	0;	Mismatches 302;	Indels	7; Gaps
3;				
QY	2247	tggcttcgatagcgcagatgaatactctcttgatgataaatatgaaccttcaactgtga	2306	
Db	8	TGGGTCGTATAGCAGCAAGATGCCCATCGATCAACTATGAGAAGCTCAAACCTGA	67	
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Db	128	CACCTCATGCACCACACAATGCGTATGACTTGGAAGTCATCGATATCTTTAAGATAGA	187	
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Fri Mar 8 08:31:54 2002

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